```
2,435, Ap

10,4301

45,64

45,64

35, Appl

10,29, Appl

1, Appl

62, Appl

62, Appl

64, Appl

66, Appl

66, Appl

66, Appl

66, Appl

67, Appl

68, Appl

69, Appl

60, Appl

                                                                                                                                                                          May 24, 2004, 10:35:46; Search time 51.0566 Seconds (without alignments) 358.588 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by snalysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1
Sequence 3
Sequence 3
Sequence 3
Sequence 5
Sequence 5
Sequence 5
Sequence 5
Sequence 5
Sequence 2
Sequence 2
Sequence 2
Sequence 3
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-214-808-1

US-09-10-641-35

US-09-322-91A-4504

US-09-10-641-35

US-09-134-840-3

US-09-434-840-3

US-09-434-840-56

US-08-554-612C-10

US-08-554-612C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682709 segs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 160%
Listing first 45 summaries
                                                                                                                   - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O
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18 54.5 2220 2 US-08-332-376A-3 Sequence 3, Appli 18 54.5 3700 3 US-08-391-160-22 Sequence 22, Appli 18 54.5 5410 4 US-09-223-176A-70 Sequence 70, Appl 18 54.5 5410 4 US-09-223-1760 Sequence 96, Appl 18 54.5 10399 4 US-08-961-527-160 Sequence 96, Appl 18 54.5 10399 4 US-08-961-527-160 Sequence 1, Appli 17.8 53.9 201 4 US-09-641-638-61 Sequence 1, Appli 17.8 53.9 1251 2 US-09-611-930-2 Sequence 236, Appl 17.8 53.9 1251 2 US-09-340-993-2 Sequence 2, Appli 17.8 53.9 1251 2 US-09-340-993-2 Sequence 2, Appli 17.8 53.9 1251 3 US-09-444-2 Sequence 2, Appli 17.8 53.9 1353 3 US-09-340-993-8 Sequence 3, Appli 17.8 53.9 1353 4 US-09-468-462-8 Sequence 8, Appli 17.8 53.9 1353 4 US-09-468-462-8 Sequence 8, Appli 17.8 53.9 1353 4 US-09-468-462-8 Sequence 8, Appli 17.8 53.9 1482 4 US-09-348-9039-8 Sequence 8, Appli 17.8 53.9 1482 4 US-09-468-4520 Sequence 13, Appli 17.8 53.9 1542 4 US-09-468-4520 Sequence 652, Appli 17.8 53.9 1542 4 US-09-468-6520 Sequence 652, Appli 17.8 53.9 1542 4 US-09-468-6520 Sequence 652, Appli 17.8 53.9 1542 4 US-09-641-652 Sequence 652, Appli 17.9 Equili 17.8 53.9 1542 4 US-09-641-641-641-641-641-641	ALIGNMENTS RESULT 1 U6-09-489-2435/c 1 Sequence 2435, Application U8/09469039A Patent No. 6610836 GENERAL INFORMATION TITLE OF INVENTION: PREDUMNIAB FOR DIAGNOSTICS AND THERAPETICS TITLE OF INVENTION NUMBER: US/09/489, 039A CURRENT APPLICATION NUMBER: US/09/489, 039A CURRENT APPLICATION NUMBER: US/0117,747 PRIOR APPLICATION NUMBER: US/0117,747 PRIOR APPLICATION NUMBER: US/0117,747 TENORY IN 122 TENORY: LEBNOTH: 1122 TENORY: LEBNOTH: LEBNOTH: US/09/489, 039A CORGANIEM: Klebsiella pneumoniae US-09-489-039A-2435	Y Match 60.6%; Score 20; DB 4; Length 1122; Local Similarity 82.1%; Pred. No. 9; hes 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0; 5 TCTTCTCCGAGCCGGTCGAAAAGAGCG 122 1103 TCTTCCGCGAGCGGAAATAGTGC 1076 124-808-1 ence 1, Application US/09214808A
C C 28 18 18 18 18 18 18 18 18 18 18 18 18 18	REBULT 1 UB-09-489-039A-2435 Bequence 2435, Ap. Batent No. 661081 GERERAL INPORMATI TITLE OF INVERTI TITLE OF INVERTI TITLE REFERENCE: TITLE REFERENC	Match Odal 8 8 23 5 1103 4-808-

APPLICANT: Resenthal, Andre
APPLICANT: Resenthal, Andre
APPLICANT: Resenthal, Andre
APPLICANT: Periberg, Christoph
APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVEXTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
PILER REPERENCE: CARPOSS
TITLE OF INVEXTION: Plasmid
FILE REPERENCE: CARPOSS
CURRENT PILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR PILING DATE: 1997-07-10
NUMBER OF SEQ ID NOS: 1
SOPTHARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 536165

Seguence

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Gapa ö

us-10-144-679-1.rnf

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EMERAL INFORMATION:

APPLICANT: ROWANN, JOSEPH W.

APPLICANT: SHIPTLIFF, ROXANNE

APPLICANT: WILLIAMS, KIMBERLY G.

TITLE 02 INVENTION: ISOTHERMAL AMPLIFICATION BASED ASSAY FOR

TITLE 02 INVENTION: MIP-LABETA QUANTIFICATION OF CHEMORINES RANTES,

TITLE 02 INVENTION: MIP-LABETA AND MIP-LEBETA

TORRESPONDENCE ADDRESS:

ADDRESSEE ANZO NOBEL PATENT DEPARTMENT

STREET: 1300 PICCARD DRIVE, SUITS 206

CITY: ROCKVILLE

STATE: MARLIAND

COUNTRY: USA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
WRITH TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/356,281
                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 76.7%; Pred. No. 20;
Matches 23; Conservative 0; Mismatches
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57.0%; Score 18.8; D
Best Local Similarity 76.7%; Pred. No. 20;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 Crcrectcadecadececatatagaga 13
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CLASEPECATION
PRIOR APPLICATION
APPLICATION NUMBER: 09/010,641
PRILING DATE:
PRILING DATE:
ATTORNEY/AGENT IMPORMATION:
NAME: KLESNER, SHARON N.
REGIGIFACTION NUMBER: 36,335
TELECCHUNICATION INPORMATION:
TELEPHONE: 301-948-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/09356281
Patent No. 6218154
                                                                     TELEPHONE: 301-948-7400
TELEPAX: 301-948-9751
INPOTENTION FOR 808 ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAK: 301->>> INPORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      TYPE: nucleic ac
                                                                                                                                                                                                                                             TOPOLOGY: Linear
MOLECULE TYPE: DNA
US-09-010-641-35
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MACALINE ALCONOMY, MECHANING ACID SEQUENCES RELATING TO PSEUDOMONA, TITLE OF INVENTION: ARENDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENDIANOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENDIANOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF EQ. ID NOS: 33142
LENGTH: 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/09010641

Sequence 35, Application US/09010641

Patent No. 6121023

GENERAL INFORMATION:
APPLICANT: ROWANNO, JOSEPH W.
APPLICANT: WILLIAMS, KIMBERLY G.
TITLE OF INVERTION: THE DETECTION AND QUANTIFICATION OF CHEMOKINES RANTES,
TITLE OF INVERTION: THE DETECTION AND QUANTIFICATION OF CHEMOKINES PARTES,
TITLE OF INVERTION: MIP-1APHA AND MIP-1BETA
MUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: AXZO NOBEL PATENT DEPARTMENT
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARLIAND
COUNTRY: USA
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                                                                                              Query Match 60.6%; Score 20; DB 4; Length 536165; Best Local Similarity 82.1%; Pred. No. 21; Matches 23; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.5%; Pred: No. 25;
Matches 22; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,641
FILLING DATE: 22-JAN-1998
CLASSIFICATION: 435
ATTCRNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   455880 crcrrcaccaaccacaccaaccaa 455907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1128 CAGCACTTCGCCGAGCATGTCGAAATA 1102
                                                                                                                                                                                                      4 CTCTTCTCCGAGCCGGTCGAATAGTGA 31
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                                                                                                                                                                                                                                                                                                                                                    9-09-252-991A-4504/c
Sequence 4504, Application US/09252991A
Patent No. 6531795
GENERAL INPORMATION:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa US-09-252-991A-4504
// TYPE: DNA
// ORGANISM: Rhizobium
US-09-214-808-1
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Query Match

Sert Local Similarity 72.7%; Pred. No. 40;

Matches 24; Conservative 0; Mismatches 9; Indels 0
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                                                                                                                  APPLICANT Glamebrook, Jane
APPLICANT Glamebrook, Jane
APPLICANT Jirage, Dayadevi
APPLICANT Tootle, Tina L
APPLICANT Exou, Nan
APPLICANT Exou, Nan
APPLICANT SHOU, Nan
TITLE OF INVENTION PAD4 COMPOSITIONS AND METHODS THENEFOR
FILE REFERENCE: 643503.0009
CURRENT APPLICATION NUMBER: US/09/434,840
CURRENT FILING DATE: 1999-11.04
SARLIER APPLICATION NUMBER: 09/190,733
RABLIER APLING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PALCHING OFFE: 1206: 85
SOFTWARE: PALCHING OFFE: 1206: 85
IRNGER OF SEQ ID NOS: 82
IRNGER OF SEQ ID NOS: 82
IRNGER: 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09434840

Patent No. 662085

GENERAL INFORMATION:
APPLICANT GLAZENCOK, Jane
APPLICANT TOCCIe, Tina L
APPLICANT: TOCCIe, Tina L
APPLICANT: TOCCIe, Tina L
APPLICANT: TOCCIe, Tina L
APPLICANT: ENQU, Nan
APPLICANT: PAGA
CURRENT PLILUG DIRE: 1999-11-04
CURRENT PLILUG DIRE: 1999-11-04
CURRENT PLILUG DIRE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
BOUTHARRE: Patentin Ver. 2.0
SEQ ID NO 3
LENGOTH: 1722
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                                     ; Sequence 1, Application US/09434840 ; Patent No. 6620985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPB: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) FEATURE:

// NAME/KEY: CDS

// LOCATION: (36)..(1064)

US-09-434-840-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (36)..(1616)
US-09-434-840-1
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                                                                                                                                                             Sequence. The G444799 GENERAL INPORMATION:
APPLICANT: ROSS, BILGE C.
TITLE OF INTERTION:
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORESSON & POERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: C...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.0%; Score 18.8; DB 4; Length 3182; Best Local Similarity 76.7%; Pred. No. 35; Matches 23; Conservative 0; Mismatches 7; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPARY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Comparible
COMPUTER: IBM Comparible
COMPUTER: ISM Comparible
COMPUTER: US/09/221,0178
FILLING DATE: 23-DEC-1998
CLASSIFICATION UNBER: US/09/221,0178
FILLING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA;
APPLICATION NUMBER: PPI182
PRIOR APPLICATION DATA;
APPLICATION NUMBER: PPI184
PRIOR APPLICATION DATA;
PRIOR APPLICATION NUMBER: PPI546
PLING DATE: 30-JAN-1998
PRIOR APPLICATION DATA;
PRIOR APPLICATION DATA;
PRIING DATE: 10-APR-1998
PRIOR APPLICATION NUMBER: PCT/AU98/01023
PRIOR APPLICATION NUMBER: PCT/AU98/01023
PRIORSY/ABRIT INCOMMATION:
NAME: MOILOY, GLAGYS H
REPRENCY/DOCKET NUMBER: 32,430
REPRENCY/DOCKET NUMBER: 32,430
REPRENCY/DOCKET NUMBER: 313,40-20021.CO
TELESCOMMUNICATION NUMBER: 313,40-20021.CO
TELESCOMMUNICATION NUMBER: 313,40-20021.CO
TELESCOMMUNICATION NUMBER: 313,40-20021.CO
TELESCOMMUNICATION NUMBER: 513,40-20021.CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1334 cagcicirciccaargcornearardig 1305
42 CTCTGCTCCCAGCCCCCTATAGTGAGT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: TKKNOWN
ORGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                      REBULT 6
US-09-221-017B-1029/c
; Sequence 1029, Application US/09221017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEC ID NO: 1029: SEQUENCE CHARACTERISTICS: LENGTH: 3182 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-221-017B-1029
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Gaps

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APPLICANT: Glazebrock, Jane
APPLICANT: Jitage, Dayadevi
APPLICANT: Tootle, Tina L
APPLICANT: Tootle, Tina L
APPLICANT: Ebou, Nan
APPLICANT: Ebou, Nan
APPLICANT: Epou, Nan
FILE REPRENCE: 041503.0609
CURRENT APPLICATION WHORE: 1099-11.04
EARLIER APPLICATION WHORE: 1099-11.12
NUMBER OF SEQ ID NOS: 88
SEQ ID NOS: 88
LENGTHARE: Patentin Ver. 2.0
ELENGTH: 1732
                             Application US/09434840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGNATSM: Arabidopsis thaliana
PRATURE:
NAME/KEY: CDS
1 LOCATION:
US-09-434-840-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Arabidopsis thaliana
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.74;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
f LOCATION: (1)..(1158)
US-09-434-840-60
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NAMB.KEY: CDS
CCATION: (1)..(1626)
COTHER INFORMATION: nucleotide sequence of wild type PAD4 cDNA cloned
COTHER INFORMATION: in pCR1.1
US-09-434-840-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1731;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Glazeboxok, Jane
APPLICANT: Glazeboxok, Jane
APPLICANT: Glazeboxok, Jane
APPLICANT: Glazeboxok, Jane
APPLICANT: Tootle, Tina L
APPLICANT: Evey, Bart
FILE OF INVENTION: BAD4 COMPOSITIONS AND WETHODS THEREFOR
FILE REFERENCE: 043503, 0009
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: 09/190,733
EARLIER PILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
LEMINE: LINE
                                             APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Jirage, Dayadevi
APPLICANT: Toole, Tina L
APPLICANT: Toole, Tina L
APPLICANT: Toole, Man
APPLICANT: Feys, Bart
TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
FILLE REFERENCE: 043503.0009
FILLE REFERENCE: 043503.0009
FILLE REPERENCE: 043503.0009
FILLE REPERENCE: 1999-11-04
SARLIER PILLING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
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SOFTWARE: PATCHING DATE: 1990-11-12
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SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PATCHING DATE: 1990-11-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.4%; Score 18.6; C
Best Local Similarity 72.7%; Pred. No. 40;
Matches 24; Conservative 0; Mismatches
Application US/09434840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce 54, Application US/09434840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
OKGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (1)..(1548)
US-09-434-840-62
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     DB 4; Length 1732;
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                                                                                                                                                                                                                          WG-09-434-840-60
Sequence 60. Application US/09434840
Patent No. 6620985
GERERAL INPORMATION:
Patent No. 6620985
GERERAL TOOR Glarabrook, Jane
APPLICANT: Glarabrook, Jane
APPLICANT: Toole, Tina in APPLICANT: Peys Bart
CITLE REFERENCE: 04303.0009
GURRENT PILING DATE: 1999-11-04
RAMLIER PPLING DATE: 1999-11-04
RAMLIER PILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 85
SEQ ID NOS: 06
LENGTH: 1712
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indele
                                                                                                                                1165 CAACTCTTAGCCGAGCCACTCGACATTGCGAAT 1197
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Ouery Match 56.4%; Score 18.6; D
Best Local Similarity 72.7%; Pred. No. 40;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18.6; D. Pred. No. 40; O. Mismatches
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APPLICANT: Glasebrook, Jane
APPLICANT: Glasebrook, Jane
APPLICANT: Toole, Tina L
APPLICANT: Toole, Nan
APPLICANT: Peya, Bart
TITLE OF INVENTION: PADA COMPOSITIONS AND MECHODS THEREFOR
TITLE REFERENCE: 043503.0009
CURRENT APPLICATION UNGER: US/09/434,840
CURRENT PILING AFTE: 1999-11-04
EARLIER PAPLICATION UNGER: 09/190,733
EARLIER PILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
ILLORTH: 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATION: (8796)
THER INFORMATION: n = g or a or c or
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                                                 upplication US/09434840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (7327)
OTHER INPONATION: n = g or a
PRATURE:
NAME/KEY: unsure
LOCATION: (7423)
OTHER INPORMATION: n = g or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAMB/KEY: ungure
CCATION: (8755)
YTHER INFORMATION: n = g or
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COCATION: (8774)
TTHER INFORMATION: n =
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OTHER INFORMATION: n =
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THER INFORMATION: n
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STHER INFORMATION: n
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THER INFORMATION:
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THER INFORMATION:
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THER INFORMATION:
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                                                    Sequence 5, Applicat
Patent No. 6620985
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bloksberg, Leonard, N. APPLICANT: Bloksberg, Leonard, N. APPLICANT: Lubbers, Mark W. APPLICANT: Lubbers, Mark W. APPLICANT: Lubbers, Mark W. APPLICANT: Debets, James APPLICANT: Christensson, Anna C. APPLICANT: Go'Toole, Paul W. APPLICANT: Reid, Julian R. APPLICANT: Reid, Julian R. APPLICANT: Colbear, Timochy TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: Polynucleotides, materials them. CURRENT PLINGO DATE: 2000-08-08 NUMBER OF SEQ ID NOS: 422 SOFTWARE: PaefSEQ for Windows Version 4.0 SOFTWARE: PaefSEQ for Windows Version 4.0 SEQ ID NO 20 LENGTH: 7213
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US-09-434-840-58

US-09-434-840-58

Sequence 58, Application US/09434840

PREMENT NO. 6620985

GENERAL INPORMATION:
APPLICANT: Clarabrook, Jane
APPLICANT: Coctle, Tina L
APPLICANT: Coctle, Tina L
APPLICANT: Evot. Bart
ITLE APPLICANT: Pays, Bart
ITLE OF INVENTION: PAAC COMPOSITIONS AND METHODS THEREPOR
FILE REPERRACE: 045503.0009
CURRENT PILITG DATE: 1999-11-04
EARLIER APPLICATION NUMBER: 09/190,733
RALIER PILING DATE: 1998-11-12

NUMBER OF SEQ ID NOS: 85

LENGTHARE: PATENTIN VOF. 2.0

SEQ ID NO 58

LENGTH 1733

TWO 58
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56.4%; Score 18.6; DB 4; Length 7213;
Best Local Similarity 72.7%; Pred. No. 49;
Matches 24; Conservative 0; Mismatches 9; Indels 0
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US-09-634-238-20
; Sequence 20, Application US/09634238
; Detent No. 6544772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; CACANISM: Lactobacillus rhamnosus US-09-634-238-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glenn, Matthew
Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i NAME/XZY: CDS
i LOCATION: (1)..(546)
US-09-434-840-58
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GREARAL 1948/C
| Bequence 1048, Application US/09252991A
| Patent No. 6527795
| Patent No. 6527795
| Patent No. 6527795
| TURLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: MUMBER: US/09/252,991A
| CURRENT PILING DATE: 1999-02-18
| PRIOR FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SAG ID NO 1048
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Patent No. 5747660
GBNERAL INFORMATION:
APPLICANT: O'LICKY, David
TITLE OF INVENTION: RECEPTOR REC'ILATORY
TITLE OF INVENTION: REC'EIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CONTREPONDENCE ADDRESS:
ADDRESSE: 1200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
FILING DATE: No. 5747660ember 6, 1995
CIABGIPTCATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Shervood, Pamela
                                                                                                                                                                                             .;
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Best Local Similarity 78.6%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 6;
                                                                                                                                            DB 4;
                                                                                                                                         Guery Match
Best Local Similarity 78.6%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                           1209 chrcrccrcccachecachecrcchachae 1182
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                                                                                                                                                                                                                                            1 CATCTCTCTCCGAGCCGGTCGAAATAG 28
                                           TYPE: DNA
) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Menlo Park
STATE: Callfornia
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy di
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US-08-554-612C-12
SEC ID NO 1087
LENGTH: 1236
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Sequence 1087, Application US/09252991A
Sequence 1087, Application US/09252991A
Sequence 1087, Application US/09252991A
Sequence 1087, Application
TITLE OF INVENTION:
TITLE OF INVENTION: ARRUINOSA POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUINOSA POR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBAGE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (5637)..(5816)

OTHER INFORMATION: Sequence of Zinc Pinger Homology Region
Patent No. 6620985
US-09-434-840-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3943 caacitciraaccaaaccacicaacairaccaar 3975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.4%; Score 18.6; Di
Best Local Similarity 72.7%; Pred. No. 52;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (10384)
OTHER INFORMATION: n = g or a or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (3070).. [4407)
OTHER INFORMATION: Second Exon of PAD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1722)..(1967)
OTHER INFORMATION: First Exon of PAD4
  gor a or c
                                                                                                                                                                                                                                                                     LOCATION: [10289]
OTHER INFORMATION: n = g or a or c
                                                                                                                                            NAME/KEY: unsure
LOCATION: (10178)
OTHER INFORMATION: n = g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (10382)
THER INFORMATION: n = 9 or
                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (10322)
OTHER INFORMATION: n = g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION: (10360)
INFORMATION: n * 9 or
  OTHER INPORMATION: n
                                                                          CATION: (9480)
HER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAMB/KEY: unsure
LOCATION: (10372)
OTHER INFORMATION:
                                                                                                                                                                                                                                               NAME / KBY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                               KBY: unsure
                                                                                                                                                                                                                                                                                                                                                  AMB/KBY: ungure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAMB/KEY: CDS
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REGULT 20
US-08-554-612C-10
Sequence 10, Application US/08554612C
Sequence 10, Application US/08554612C
Sequence 10, Application US/08554612C
STATES OF INVENTION:
TITLE OF INVENTION: PROSTENDIN F2' RECEPTOR REGULATOR:
TITLE OF INVENTION: PROSTENDIN PROTEIN AND THERAPRUTIC USES
CORRESPONDENCE ADDRESS:
STREET: 2200 ABDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.6%; Pred. No. 53;
Matches 22; Conservative 0; Mismatches 6; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08554612C
PRETENT NO. 5747660
GENERAL INFORMATION:
APPLICANT: Orlicky, David
TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
TITLE OF INVENTION: PROSTEIN AND THERAPBUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDING ADDRESS:
ADDRESSEE: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: ALTO SAUGHT MORG, SULLE TOO
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
ZIP: 94025
COMPUTER RADABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPy disk
COMPUTER: PROPERING PC-DOS/MS-DOS
SOPTAMRE: PatentIn NUMBER: US/08/554,612C
71LING DATE: NO. 5747660mber 6, 1995
CLASSIPICATION NUMBER: 36,677
RETERPONE: SAB-TOCKET NUMBER: 36,677
RETERPONE: (415) 312-5070
TELECOMMINICATION INPORMATION:
TELECOMINICATION INPORMATION:
TELECOMMINICATION INPORMATION:
TELECOMMINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Menio Park
STATE: California
CCUNTRY: U.S.A.
ZIP: 94025
CCMPUTER READABLE PORM:
WEDIOM TYPE: Ploppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1606 ArgrerrerceAddecestaAcArarr 1633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ropology: linear
MOLECULE TYPE: CDNA
U9-08-554-612C-10
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US-08-554-612C-11
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Patent Mo. 5747660

GENERAL INFORMATION:
APPLICANT: O'LICAY, David
ITILE OF INVENTION: PROBTAGLANDIN F2' RECEPTOR REGULATORY
ITILE OF INVENTION: PROBTAGLANDIN F2' RECEPTOR REGULATORY
ITILE OF INVENTION: PROBTAGLANDIN F2' RECEPTOR REGULATORY
INVERTER O'LICAY: RECEPTOR REGULATORY
CORRESPONDENCE ADDRESS:
STREET: SALON Sand Hill Road, Suite 100
CITY: Mandlo Park
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 78.64; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 6; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.4; DB 1; Length 2898; Pred. No. 53; 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/554.612C
FILLIAG DATE: Wo. 574660ember 6, 1995
CLASSIFTCATION: 536
ATTORNST/AGANT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 06519/004001
TELEPHONE: (415) 854-0875
TELEPHONE: (415) 854-0875
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LEGGTH: 2898 base pairs
TYPE: nucledc acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1606 ArgrericrecaAccecrereachian 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1595 Argrichiciandececricandary 1622
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                                                           06519/004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   TELEPORTUNICATION INPORTATION OF TELEPACH (415) 322-5070
TELEPACH (415) 854-0875
INPORMATION FOR SEQ ID NO. 12: SEQUENCE CHARACTERISTICS:
                      REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 78.6%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HOLECULE TYPE: CDNA
US-08-554-612C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
Titla OF INVENTION: WICLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLA OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILS REPERENCE: 2709.2004/01
FILS REPERENCE: 2709.2004/01
CURRENT PELING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117.747
NUMBER OF SEQ ID NOS: 14342
ENGILL OF SEQ ID NOS: 14342
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                                                                                                                                    US-09-489-039A-1572/C
US-09-489-039A-1572, Application US/09489039A

### Patent No. 6610836

### GARRAL INPORMATION:
### PAPLICANT: GARRATION:
### PILK OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
### PILK OF INVENTION: NUMBER: 08/09/489,039A

### CURRENT FILING DATE: 2000-01-27

### PRIOR PAPLICATION NUMBER: US 60/117,747

### PRIOR PAPLICATION NUMBER: 1999-01-29

### NUMBER OF 8EQ IN NOS: 14342

### SEQUENCES RELATING
### PILK PAPLICATION NUMBER: US 60/117,747

### NUMBER OF 8EQ IN NOS: 14342
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Best Local Similarity 80.84; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 checherricaceerecceeresnearaecea 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.2%; Score 18.2; D
Best Local Similarity 74.2%; Pred. No. 53;
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INPORMATION:
APPLICANT: Highfield, Peter Edmund APPLICANT: Rodgers, Brian Colin APPLICANT: Tedder, Richard Seron APPLICANT: Barbare, John Anthony James TITLE OF INVENTION: Viral Agent NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TCTCCGAGCCGGTCGAAATAGTGAGT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3807, Application US/09489039A Patent No. 6610836
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08191160; Patent No. 6210675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Klebsiella pneumoniae US-09-489-039A-1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-489-039A-3807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ਜੰ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 5843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.8%; Score 18.4; DB 1; Length 2909; Best Local Similarity 78.6%; Pred. No. 53; Matches 22; Conservative 0; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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SEQUENCE 2, ABDIICATION US/08554612C

GENERAL INFORMATION:
APPLICANT: OTILCKY, David
TITLE OF INVENTION: PROFINGLANDIN F2' RECEPTOR REGUL
TITLE OF INVENTION: PROFINGLANDIN F2' RECEPTOR REGUL
TITLE OF INVENTION: PROFIER AND THERAPEUTIC USES
NUMBER OP SEQUENCES: 51
CORRESPONDENCE High & Richardson P.C.
STREBER OP SEQUENCES: 51
COUNTRY: Wenlo Park
STREBE: California
COUNTRY: U.S.A.
ZIP: 94025
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE PORN:
WEDIUM TYPE: Ploppy disk
COMPUTER READABLE PORN:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE PORN:
MEDIUM TYPE: Ploppy disk
COMPUTER: U.S.A.
ZIP: 94025
COMPUTER READABLE PORN:
MEDIUM TYPE: Ploppy disk
COMPUTER: BENEADABLE PORN:
MEDIUM TYPE: PLOPPY disk
COMPUTER: BENEADABLE PORN:
MEDIUM TYPE: PLOPPY DISK
COMPUTER: AND PROFIL NO STATOGOMBER 6, 1995
COMBUTERTION NUMBER: SECTION
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 06519/004001
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
FILING DATE: NO. 5747660ember 6, 1995
CLASSIFICATION: 536
ATTOMNEY AGENT INPORMATION:
NAME: Sherwood, Panela
REGISTRATION NUMBER: 36,677
REGISTRATION NUMBER: 36,677
TELEBRACHONICATION INPORMATION: (415) 312-5070
TELEBRACH (415) 312-5070
TELEBRACH (415) 312-5070
TELEBRACH (415) 312-5070
TELEBRACH (415) 312-5070
TEMERATION POR SEQ ID NO: 11: SEGUENCE CHARACTERISTICS:
LENGTH: 3099 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Natch 55.8%; Score 18.4; D
Best Local Similarity 78.6%; Pred. No. 58;
Natches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1606 ArgicirciccaAgcccgrcaAcaiarr 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ATCICITCICCGAGCCGGICGAAAIAGT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAK: (415) 654-0875
INPORMATION FOR EED ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5843 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
HOLECULE TYPE: CDNA
US-08-554-612C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
US-08-554-612C-2
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2 ATCTCTTCTCCGAGCCGGTCGAAATAGT 29

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Highlield, Peter Edmucd
APPLICANT: Tedder, Stchard Seton
APPLICANT: Tedder, Stchard Seton
APPLICANT: Tedder, John Anthony James
TITLE OF INVENTION: Viral Agent
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg. Ernst & Kurz
STREET: 1700 K Street
CITY: Washington
COUNTRY: U.S.A.

COUNTRY: U.S.A.

CONDITER: 19006
COMPUTER FALDALE PORM:
MEDLING TYPE: 190ppy diskette, 5.25 inch, 360 Kb storage
COMPUTER: 180A AT compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.5%; Score 18; DB 2; Length 1176; Best Local Similarity 80.8%; Pred. No. 70; Astches 21; Conservative 0; Kiematches 5; Endele
IMPROVED HCV DIAGNOSTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INPORMATION: KHCV N95-1.2, Fig. 3
US-08-537-811-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPOTER: IBM Compatible
COMPOTER: IBM Compatible
COMPATER: IBM Compatible
SOFTAME: PRESENT DOS
SOFTAME: PRESENT NAME
APPLICATION NUMBER: US/08/537,811
FILING DATE: 24-057-1995
CLASSIPPICATION (435
PALOR APPLICATION NUMBER: PCT/KR94/00040
PILING DATE: 29-APR-1994
APPLICATION NUMBER: KR 93-7440
FILING DATE: 30-APR-1994
APPLICATION NUMBER: RR 93-7440
FILING DATE: 10-APR-1994
ATCORNEY/AGENT INPORMATION:
NAME: ACCORDANCE TO THE NAME ATCORDANCE TO THE NAME ATTORDANCE TO THE NAME ATCORDANCE TO THE NAME ATCORDANCE TO THE NAME ATTORDANCE TO THE NAME ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jones, III, Harry C
REGISTATION NUMBER: 20.280
REFERENCE/DOCKST NUMBER: 8512-037-999
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480 crccecrcesascescrceanasan 455
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                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08191160 Patent No. 6210675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
             TITLE OF INVENTION: IMPRITIES OF SEQUENCES: 48
CORRESPONDENCE ADDRESSE:
ADDRESSE: Pennie & EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear HOLECULE TYPE: CDN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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LOCATION: polyprotein
GTHER INFORMATION: probably encodes viral non-structural
GTHER INFORMATION: proteins
US-08-191-160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 54.5%; Score 18; DB 3; Length 1035; Best Local Similarity 80.8%; Pred. No. 68; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                        ZIP: 20006
COMPUTBR READABLE FORM:
MEDIUM TYPE: Flopy diskette, 5.25 inch, 360 Kb storage
COMPUTBR: IBM AT compatible
OPERATING SYSTEM: MS-DOS V3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: human; serum infectious for PT-NANBH
INMEDIATE SOURCE:
LIBRARY: clone JG3 from cDNA library in lambda gtll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1035 base pairs
TYPE: nucleotide with corresponding protein
STRANDEDNESS: single
                                                       , Pigg, Brnst & Kurz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PLING DATE: 17 DEC 1990
APPLICATION NUMBER: UK 89 28 562.1
PLING DATE: 18 DEC 1989
PLING DATE: 18 DEC 1989
PRIOR APPLICATION NUMBER: UK 90 04 414.0
PLING DATE: 37 RBB 1990
PRIOR APPLICATION DATA: 4PLICATION DATA: 4PLICATION DATA: 4PLICATION NUMBER: UK 90 04 814.1
PRIOR APPLICATION NUMBER: UK 90 04 814.1
PRIOR APPLICATION NUMBER: 1990
ATTORNEY/AGENT INPORMATION:
NAME: B. ARTHONY F199
ATTORNEY/AGENT INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELESPAX: (202) 833-5740
TELESPAX: (202) 833-5744
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
CONTINUED TO THE SECOND TO T
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect 5.0 (DOS LEXT)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,160
FILLIG DATE:
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US-08-537-811-41/c

9 Sequence 41, Application US/08537811

Patent No. 5910405

GENERAL INFORMATION:
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CHOI, DEOG YOUNG
KIM, CHUN HYUNG
SO, HONG SEOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YANG, JAB YOUNG
KIM, IN SOO
KIM, JOO HO
                                                  Rothwell, F
                                                                                       STREET: 1700 K S
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
APPLICANT
APPLICANT
APPLICANT
APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: U.S.A.
ZIF: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette, 5.25 inch, 360 Kb storage
COMPUTER: IEBM PC compatible
OPERATING SYSTEM: PC-DOS MIS-DOS
SOPTWARE: PACEMENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,376A
FILING DATE: 17-SEP-1997
CLASSIPICATION: 435
ATTORNEY/AGENT INPOMMATION:
NAME: SAVIENCY, Thomas R.
REGISTRATION NUMBER: 31,661
REFERENCE COCKET NUMBER: 0010144a
TELECHONE: (609) 252-4526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2220 beas pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1700 K Street CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: TADDY LIBACICE, 5.25 INCOMPUTER: IBM AT COMPATIBLE

OPERATING SYSTEM: MS-DOS V3.2

SOFTWARE: Wordperfect 5.0 (DOS text)

CURRENT APPLICATION DATA:

PILING DATE:
CLASSIPTCATION:
PRICK APPLICATION DATA:

APPLICATION NUMBER: U5/028,516

FILING DATE: 17 DEC 1990

APPLICATION NUMBER: U7 89 28 562.1

FILING DATE: 18 DEC 1989

PRICK APPLICATION DATA:

PRICK APPLICATION DATA:

PRICK APPLICATION DATA:

FILING DATE: 18 DEC 1989

PRICK APPLICATION DATA:

PRICK APPLICATION DATA:

PRILING DATE: 27 PEB 1990

PRICK APPLICATION DATA:

PRILING DATE: 03 MAR 1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1344 rrcrecaacccearcaacagreag 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Highfield, Peter Edmund.
APPLICANT: Redgers, Brian Colin
APPLICANT: Tedder, Richard Seton
APPLICANT: Barbara, John Anthony James
TITLE OF INVENTION: Viral Agent
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TICTCCGAGCCGGTCGAATAGTGAG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08191160
Patent No. 6210675
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-932-376A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -191-160-22/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: from 1 to 1770 bp portion of the PT-NAMBH
LOCATION: polyprotein probably encodes viral non-structural
OTHER INFORMATION: proteins
US-08-191-160-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 54.5%; Score 18; DB 3; Length 1770; Best Local Similarity 80.8%; Pred. No. 74; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: clone JG2 from cDNA library in lambda gtil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Politino, Michael
APPLICANT: Tonzi, Sean M.
APPLICANT: Usher, John J.
APPLICANT: Burnett k, William V.
APPLICANT: Romandik, Guna
TITLE OF INVENTION: CEPHALOSPORIN ESTERASE GENE PROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECTLE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: human; serum infectious for PT-NANEH
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1770 base pairs
TYPE: nucleotide with corresponding protein
STRANDEDNESS: single
                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/628,516
FILING DATE: 17 DEC 1990
APPLICATION NUMBER: UK 89 28 562.1
FILING DATE: 18 DEC 1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UK 90 04 414.0
FILING DATE: 27 FEB 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 90 04 814.1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 90 04 814.1
FILING DATE: 03 602 1990
ATTORNEY/AGENT INPORMATION:
NAME: E ARTHORY PIGG
REGISTRATION NUMBER: 27,195
REGISTRATION NUMBER: 27,195
REGISTRATION NUMBER: 27,195
REGISTRATION NUMBER: 27,195
TELECROMUNICATION INPORMATION:
TELECROMUNICATION INPORMATION:
TELECROMUNICATION SEG 10 NO: 3:
SEQUENCE CHARACTERISTICS:
TRUGTH: 1770 Dass pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Briscol-Myers Squibb Company
STREET: Rt. 206 & Provinceline Road
CITY: Princeron
STATE: New Jersey
  OPERATING SYSTEM: MS-DOS V3.2
SOFTWARE: Wordperfect 5.0 (DOS text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CTCTTCTCCGAGCCGGTCGAAATAGT 29
                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08932376A Patent No. 5869309 GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Bristol-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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ઠે 윱 NAME: R. Anthony Figg RECISTRATION NUMBER: 27,195

ZIP: 08543-4000 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

USA

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YANG, Jae Young
TITLE OF INVENTION: HEPATITIS C DIAGNOSTICS AND VACCINES
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.5%; Score 18; DB 4; Length 5410; Best Local Similarity 80.8%; Pred. No. 86; Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Dasjeon
CITY: Dasjeon
COUNTRY: Rapublic of Korea
ZIP: 365-340
COMPUTER READBLE FORM
COMPUTER: READBLE FORM
COMPUTER: IBM PC/pentium
COMPUTER: IBM PC/pentium
COMPUTER: Mindows
SOFFWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESER: YANG, Jae Young
ETREET: 386-1, Doryong-dong, Yuseong-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/150,2048
FILING DATE: 20-Apr-1994
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 2695/FLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4186 retrerecedacecercedacreare 4211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUBER: KR 91-9510
FILING DATE: 10-JUN-1991
APPLICATION NUBER: KR 91-13601
FILING DATE: 6-AUG-1991
                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Shaban Islam, Esq.
REGISTRATION NUMBER: 32,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UG-08-IS0-204E-96/c
; Sequence 96, Application UB/08150204B
; Parent No. 6538126
; GENERAL INFORMATION:
; APPLICANT: CHD, Joong Myung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAX: (212) 940-8776
INFORMATION FOR SEQ ID NO: 96
SEQUENCE CHARACTERISTICS:
LENGTH: 9472 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young Woo
Kook Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                NAME/KET: misc_feature
) LOCATION: 1...5410
US-09-221-017B-70
                                                                                                                                                                                                                       ANTI-SENSE: UNKNOWN
                     INFORMATION FOR
SEQUENCE CHARA
LENGTH: 541
                                                                                                                                                                                                                                                                                               PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bequence 70, Application US/09221017B
Patent No. 6444799
GENBRAL INFORMATION:
APPLICANT: DOBS: Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & PORRSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

S4.54; Score 18; DB 3; Length 3750;
Best Local Similarity 80.84; Fred. No. 82;
Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                             IOCATION: from 1 to 3750 bp portion of the PT-NAMBH LOCATION: polyprotein of the PT-NAMBH OTHER INFORMATION: viral non-structural proteins US-08-191-160-22
                                                                                                                                                                                                                                                                                     ORGANISM: human; serum infectious for PT-NANBH INMEDIATE SOURCE:
LIBRARY: cDNA clones from 3' end of the genome
                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3750 base pairs
TYPE: nuclectide with corresponding protein
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows
SOFTWARE: PREFESO for Windows Version 2.0b
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,0178
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27340-20021.00
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PRIOR APPLICATION NUMBER: PE2911
FILING DATE: 05-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CTCTTCTCCGAGCCGGTCGAAATAGT 29
                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA to genomic RNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
REPERENCE/DOCKET NUMBER: 1
TELECOMOUNICATION INFORMATION
TELEPHONE: (202) 833-5740
TELEPAX: (202) 833-5744
INFORMATION POR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPERENCE/DOCKET NUMBER: 2
PELECOMMILCATION INFORMATION
TELEPHONE: 650-813-5600
TELEPAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
COMPUTER READMALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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Parent No. 643548

Parent No. 643548

Parent No. 643548

GRNEAL INPORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chan, Annick

TITLE OF INVENTION: BALLELLC WARKERS DERIVED FROM GENOMIC REGIONS CARRYING

FILE REPERRORG: GENES INVOLVED IN ANACHIDONIC ACID METABOLISM

FILE REPERRORG: GENES INVOLVED IN ANACHIDONIC ACID METABOLISM

FILE OF INVENTION: GENES INVOLVED IN ANACHIDONIC ACID METABOLISM

CURRENT PELLING DATE: 0000-00-16

CURRENT PILLING DATE: 2000-00-16

PRIOR PILLING DATE: 1999-05-07

PRIOR PILLING DATE: 1999-03-03

PRIOR PILLING DATE: 1999-03-03

PRIOR PILLING DATE: 1999-03-03

PRIOR PILLING DATE: 1999-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.8%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 5; Indels
                        APPLICANT: Leitner, Brnst
APPLICANT: Geneider, Elisabeth
APPLICANT: Geneider, Elisabeth
APPLICANT: Geneider, Elisabeth
APPLICANT: Geneider, Kurt
APPLICANT: Weber. Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEGURENCES: G
CORRESPONDENCE ADDRESS:
ADDRESSES: No. 5827706artis Corporation
GITY: Bast Manover
SINTE: No. 5827706artis Corporation
GITY: Bast Manover
SINTE: No. 5827706artis Corporation
GITY: Bast Manover
SINTE: No. 5827706artis Compatible
OCHTUTE: LEM PC COMPATION
MEDION TYPE: Ploppy disk
COMPUTER: LEM PC COMPATION
OCHTUTEN: TEM PC COMPATION
OCHTUTEN: ADDRESSES: 26,389
FILING DATE: OG-UNN-1995
CLASSIFICATION NUMBER: 100-8029/CONT/CONT
TELECOMMINICATION NUMBER: 100-8029/CONT/CONT
TELECOMMINICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11867 CAGATCGTCTCCAAGCCGGTCGATAT 11842
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ORGANISM: Tolypocladium niveum STRAIN: ATCC 34921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
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US-081-57-1-50/C
US-081-57-1-50/C
US-081-57-1-50/C
Sequence 160, Application US/08361527
Patent No. 6420135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
STREST: 4010 Key West Avenue
CITTS: ROCKVILLE
COUNTY: USA
ZIP: AND KEY WEST Avenue
COUNTY: USA
ZIP: ASADABLE PORM:
MEDION TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HE Vectra 466/33
CORPUTER: HE VECTRA 466/33
COUNTY APPLICATION DATA:
SOFTWARE ASCIT FARE
SOFTWARE ASCIT FAR
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54.5%; Score 18; DB 4; Length 10399;
Best Local Similarity 80.8%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Length 9472
                                                                                                                                                                  PEATURE:
OTHER INPORMATION: MICV-LBC1, Fig. 2
SEQUENCE DESCRIPTION: SEQ ID NO: 96
US-08-150-2048-96
                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 54.5%; Score 18; DB 4; Best Local Similarity 80.8%; Pred. No. 93; Natches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1401 CTTCTCCTAGCTGATCGATATACTGA 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CTCTTCTCCGAGCCGGTCGAAATAGT 29
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION, NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 96347
TELECOMOUNICATION INFORMATION:
TELEPRACE (301) 309-8512
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 10799 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
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US-08-471-119A-1/c
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LOCATION: 510
LOCATION: 510
LOCATION: 510
LOCATION: 10-507-170 : polymorphic base A or 3
NAME/KEY: also binding
LOCATION: 481.500
JOTHER INPORMATION: 10-507-170 mis1, potential
NAME/KEY: also binding
LOCATION: 502.51
JOCATION: 502.51
JOCATION: 502.51
JOCATION: 322.35
JOCATION: 322.35
JOCATION: 739.75
JOCATION: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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; Patent No. 5962265
; GRMERAL INPORMATION:
APPLICANT: Tyrell B. No. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: Pilliam Craig Moore
TITLE OF INVENTION: BILDeretein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: BILDERETEIN
TITLE OF INVENTION: BURNISHTREBONINE KINASE
FILE REFERENCE: PHM. 70296
CURRENT FILING DATE: 1998-12-15
SEALIER PILLING DATE: 1999-12-15
HARLIER PILLING DATE: 1997-12-19
SEALIER PILLING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
SOUTH NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 CACCICITCIACCARAGGAIGACATAGTGA 517
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83.9%, Score 17.8, D
Best Local Similarity 75.9%, Pred. No. 86,
Matches 22, Conservative 0, Mismatches
                                                     PRIOR APPLIANCE
PRIOR TILING DATE: 2000.
PRIOR TILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-03-23
PRIOR PLICATION NUMBER: US 60/119,917
PRIOR PLICATION DATE: 1999-02-12
PRIOR PLICATION NUMBER: US 60/119,917
PRIOR PLICATION NOME 1304
SOFTWARE: Patent.pm
**LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TCTTCTCCGAGCCGGTCGAAATAGTGAGT 33
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CRGANISM: Homo sapiens
US-09-211-930-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chem. Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
53.94; Score 17.8; DB 4; Length 47;
Best Local Similarity 71.04; Pred. No. 54;
Matches 22; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele

LOCATION: 24

COMBINE INFORMATION: 10-507-170 : polymorphic base A or G
US-09-641-638-1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 296. Application US/09621976
PREENT NO. 6639063
GENERAL INFORMATION:
PREIGCANT: Dumas Milne Edwards, J.B.
APPLICANT: Johnest, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
PILE REFERENCE: GENEET. 054PR2
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CACCICITATION OF THE TOTAL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 611, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 1999-02-1914 PRIOR FILIAGO DATE: 1999-02-1914 PRIOR FILIAGO DATE: 1999-02-1914 PRIOR PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapiens
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NAME/KEY: sig_peptide
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LENGTH: 201
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Search completed: May 24, 2004, 12:31:17 Job time: 53.0566 secs
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APPLICANT: TYCELLE:
APPLICANT: TYCELLE:
APPLICANT: TYCELLE:
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
GURENT: DAVIG Shay Silberfetein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THRONINE KINASE
FILE REFERENCE: PHM. 70296.N1
CURRENT PLING DATE: 1999-12-21
KARLIER PLING DATE: 1999-06-25
EARLIER PLING DATE: 1999-06-25
EARLIER PLING DATE: 1999-12-15
EARLIER PLING DATE: 1990-12-15
EARLI
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APPLICANT: TYZELI B. No. 6034228ris
APPLICANT: David Shay Silbozerein
TITLE OF INVENTOR: SURMY SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REPERENCE: PRN. 70296.N1
CURENT APPLICATION NUMBER: US/99/340,993
CURENT APPLICATION NUMBER: GB 972681.0 & US 09/211,930
EARLIER APPLICATION NUMBER: GB 972681.0 & US 09/211,930
EARLIER PILING DATE: 1997-12-19 & 1998-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FestSEQ for Windows Version 3.0
LENGTH: 1251
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Bast Local Similarity 75.9%, Pred. No. 96,
Matches 22, Conservative 0, Mismatches 7, Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 TCTTCTTCGAGCTGGTCCATTTGATGAGT 355
327 TCTTCTTCGAGCTGGTCCATTTGATGAGT 355
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Patent No. 6300098
GENERAL INFORMATION:
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Patent No. 6034228
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US-09-211-930-8
; Sequence B, Application US/09211930
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CORGANISM: Homo sapiens
US-09-340-993-2
                                                                                                                                                                                 RESULT 38
US-09-340-993-2
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APPLICANT: Tyrell B. No. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERIEM/THREONINE KINASE
FILE REPERENCE: PHM. 70296
CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT APPLICATION NUMBER: US/07/211,930
RAMLIER PILLING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
SOFTTARE: EastSEG for Windows Version 3.0
SEQ ID NO 8
LENGTH. 1353
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53.9%; Score 17.8; Dest Local Similarity 75.9%; Pred. No. 87; Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 TCTTCTCCGAGCCGGTCGAATAGTGAGT 33
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
US-09-211-930-8
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May 24, 2004, 11:41:02; Search time 199.245 Seconds (without alignments) 752.721 Million cell updates/sec
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GenCore version 5.1.6
Copyright [c) 1993 - 2004 Compugen Ltd.
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33
1 catetetetecgagecggtegaaatagtgagt 33
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	1, Appli	Appl	Appli	Appl	21, Appl	Appl	Appli							
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Segmence						
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	IS-10-144-679-1	US-10-144-679-82	JS-10-144-094-1	19-10-144-094-82	US-10-144-679-87	15-10-144-679-20	JS-10-144-094-20	18-10-144-679-18	JS-10-144-679-19	18-10-144-094-18	JS-10-144-094-19	19-10-144-679-21	19-10-144-094-21	JS-10-144-679-7
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Query Match Length DB	33	33	33	33	33	20	20	20	20	20	20	20	20	 E
Query Match	100.0	100.0	100.0	100.0	95.2	84.2	84.2	80.0	80.0	80.0	80.0	72.7	72.7	66.1
Score	33	33	33	33	31.4	27.8	27.8	26.4	26.4	26.4	26.4	5	5	21.8
Result No.		71	m	*	ហ	9	7	8	σ,	10	11	12	13	7.

RESULT 2
US-10-144-679-82
US-10-144-679-82
; Sequence 82, Application US/10144679
; Publication No. US20030215810A1
; GENERAL INFORMATION:

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TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
FRATUR:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric
OTHER INFORMATION: Substrate
FRATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric
US-10-114+034-82
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US-10-144-679-20

Sequence 20, Application US/10144679

Fublication No. US20030215810A1

Fublication No. US20030215810A1

SEPLICANT: LU, YI

APPLICANT: LU, YI

TITLE OF INVENTION: COLOR CHANGES

FILE REFERENCE: 9800240-0019

CURRENT APPLICATION UNBER: 2002-05-10

CURRENT PILLING DATE: 2002-05-10

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 20

LENGTH: 50

FURNALE: SOFTWARE: SOFTW
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US-10-144-679-87

Sequence 87, Application US/10144679

Publication No. US20030215810A1

GENERAL INFORMATION:

APPLICANT: LU, VITEMEN

ITILE OF INVENTION: SIMPLE CALANITIC DNA BIOSENSORS FOR IONS BASED CN

ITILE OF INVENTION: COLOR CHANGES

FILE REFERENCE: 9800240-0019

GURRENT APPLICATION UNDERS: US/1c/144,679

CURRENT APPLICATION UNDERS: US/1c/144,679

CURRENT PILING DATE: 2002-05-10

NUMBER OF SEQ ID NOS: 86

SOOTWARE Patentin Ver. 2.1

SEQ ID NO 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; Score 33; DB 17; Length 33; I Similarity 100.0%; Pred. No. 8.9e-06; 33; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATCTCTCCCGAGCCGGTCGAAATAGTGAGT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
OKGANISM: Artificial Sequence
                                                                                                                        SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 82 LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric of THER INFORMATION: substrate
US-10-144-679-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric OTHER INFORMATION: substrate
TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON TITLE OF INVENTION: COLOR CHANGES TITLE OF INVENTION: COLOR CHANGES TITLE OF INVENTION: COLOR CHANGES CURRENT APPLICATION NUMBER: US/10/144,679 CURRENT PILLNG DATE: 2002-05-10 NUMBER OF BCQ ID NOS: 88 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 82 LEAGHH: 33 TYPES
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OGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Trans-cleaving
1. OTHER INFORMATION: deoxyriboxyme 178
US-10-144-094-1.
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UB-10-144-094-1
UB-10-144-094-1
Sequence 1, Application US/10144094
Publication No. US20040023216A1
GENERAL INPORMATION:
APPLICANT: LIU, JUBMEN
TITLE OF INVENTION: NEW FLUORESCENCE BASED BIOSENSOR
FILE OF INVENTION: NEW FLUORESCENCE BASED BIOSENSOR
CURRENT APPLICATION NUMBER: US/10/144,094
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ 1D NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO:
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Publication No. US20640023216A1
CENERAL INFORMATION:
APPLICANT: LU, YI
APPLICATION NUMBER: US/10/144,094
CURRENT PILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 84
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Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 33; Conservative 0; Xismatches 0;
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US-10-144-094-82
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APPLICANT: LU, YI

APPLICANT: LU, YI

TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FCR IONS BASED ON TITLE OF INVENTION: COLOR CHANGES

FILE REPERRICE: 9800240-0019

CURRENT PILING DATE: 2002-05-10

NUMBER OF SEQ ID NOS: 88
SOFTWARE: PATERIEIN Ver. 2.1

SEQ ID NO 19
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US-10-144-094-18
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APPLICANT: LU, YI
FILS RETREMCE: LO32Z/4
FILS RETREMCE: 1032Z/4
CURRENT APLICATION NUMBER: US/10/144,094
CURRENT APLICATION NUMBER: 2002-05-10
NUMBER OF SEQ ID NOS: 84
SOFTWARE: 90
FILM PACE: 2002-05-10
SEQ ID NO: 8
LENGTH: 50
TYNO: 1
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TITLE OF INVENTION: NEW PLUGRESCENCE BASED BIOSENSOR
PILE REPERENCE: 10322/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 80.0%; Score 26.4; DB 16; Best Local Similarity 96.4%; Pred. No. 0.013; Matches 27; Conservative 0; Mismatches 1;
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APPLICANT: LU, XI
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ORGANISM: Artificial Sequence
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US-10-144-094-18
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TITLE OF INVENTION: SIMPLE CATALITIC DNA BIOSENBORS FOR IONS BASED ON
TITLE OF INVENTION: COLOR CHANGES
FILE REPERENCE: 9800240-0019
CURRENT PELICATION NUMBER: US/10/144,679
CURRENT PILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin Ver. 2.1
EEQ ID NO 18
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Zn-DNA
US-10-144-679-20
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                                                                                       Query Match

84.2%; Score 27.8; DB 16; Length
Best Local Similarity 93.5%; Pred. No. 0.0028;
Matches 29; Conservative 0; Mismatches 2; Indels
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APPLICANT: LU, YI
TILLE OF INVENTION: NEW FLUCRESCENCE BASED BIOSENSOR
FILE REPERENCE: 10322/44
CURRENT APPLICATION NUMBER: US/10/144,094
CURRENT PILLING DATE: 2002-05-10
NUMBER OF SEQ 1D NOS: 84
SOFTWARE: PARENTEN VEF. 2.1
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84.2%; Score 27.8; DB 17;
Best Local Similarity 93.5%; Pred. No. 0.0028;
Matches 29; Conservative 0; Mismatches 2;
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96.4%; Pred. No. 0.013;
tive 0; Mismatches 1;
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Publication No. US20030215810A1
GENERAL INFORMATION:
APPLICANT: LU, YI
                                                                                                                                                                                                                                                                                                            US-10-144-094-20
; Sequence 20, Application US/10144094
; Publication No. US20040023216Al
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 27; Conservative
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LENGTH: 50
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72.74, Score 24, DB
Best Local Similarity 100.04; Fred. No. 0.1
Matches 24; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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| Gequence 21, Application US/10144679
| Publication No. US2030215810A1
| GENERAL INFORMATION:
| APPLICANT: LU, JUNEAN
| TITLE OF INVENTION: SUMPLE CATALTIC DNA BIOSEN6ORS FOR IONS BASED ON TITLE OF INVENTION: GOLOR CHANGES
| FILE REPRENCE: 9800240-0019
| CURRENT PILING DATE: 2002-05-10
| NUMBER OF SEQ ID NAS: 88
| SEGTIMARE PETERING NATE: 2012-05-10
| SEGTIMARE PETERING NATE: 2.1
| SEG ID NO 21
| LENGTH: 50
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; OTHER INFORMATION: Description of Artificial Sequence: 2n-DNA
US-10-144-094-21
                                                                                                                                                                                             ; OTHER INPORMATION: Description of Artificial Sequence: Zn-DNA
US-10-144-094-19
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Publication No. US20040023216A1

GENERAL INFORMATION:
APPLICANT: LU, YI
APPLICANT: LU, YI
APPLICANT: LU, YI
APPLICANT: LU, YI
CURRENT APPLICANTON: NHW FUUNRESCENCE HASED BIOSENSOR
FILE REPRENCE: 10322/44
CURRENT PILING DATE: 202-05-10
NUMBER OF SEQ 1D NOS: 84
SOPTWARE: Patentin Ver. 2.1
SEQ 1D NO 21
LENGTH: 50
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CURRENT APPLICATION NUMBER: US/10/144,094
CURRENT FILING DATE: 20C2-05-10
NUMBER OF SEQ ID NOS: 84
SRQ ID NO 19
LENGTH: 50
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                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                              Sequence 7, Application US/1014679
Publication No. US20030215810A1
GENERAL INFORMATION:
APPLICANT: LU, VI
APPLICANT: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON
TITLE OF INVENTION: COLOR CHANGES
FILLE REPRENCE: 9800240-0019
CURRENT APPLICATION NUMBER: US/10/144,679
CURRENT APPLICATION NUMBER: US/10/144,679
SUPRANE: PATENT NOS: 88
SOFTWARE: PATENT NOS: 88
SOFTWARE: PATENT NOS: 82
SOFTWARE: PATENT NOS: 82
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US-10-144-679-7
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OTHER INFORMATION: Description of Artificial Sequence: Variant of
1 OTHER INFORMATION: deoxyribosyme named 1721
US-10-14-044-0
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DB 17; Length 50; 0.18;
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APPLICANT: LIU, YI
APPLICANT: LIU, YI
TITLE OF INVENTION: NEW FLUORESCENCE BASED BIOSENSOR; TITLE OF INVENTION: NEW FLUORESCENCE BASED BIOSENSOR; CURRENT RILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 84
SEQ ID NO ?
LENGTHARE: Patentin Ver. 2.1
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Best Local Similarity 78.8%; Pred. No. 2;
Matches 26; Conservative 0; Mismatches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Coldman, Barry S.
APPLICANT: Chem, Xianfeag
APPLICANT: Chem, Xianfeag
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERRICE: 38-10(52052)8
FILE REPERRICE: 38-10(52052)8
PRIOR PRILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-31
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 30964
LENGTH 771
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APPLICANT: Berks, Randy M.
APPLICANT: Clausen, ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
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SOFTWARE PaetSEQ for Windows Version 4.0
SEQ ID NO 1317
LENGTH: 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1317, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 103, Application US/10074475; Publication No. US20030092898A1; GENERAL INFORMATION;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / TYPE: DNA
/ ORGANISM: Burkbolderia cepacia
US-10-369-493-30964
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu, Ping
Recipon, Herve
Karra, Kalpana
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Sublication No. US2003033675A1

GENERAL INPORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF NICROSIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BARRESSION OF NICROSIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BARRESSION OF NICROSIAL PROPERTIES
TITLE OF INVENTION: BARRESSION OF NICROSIAL PROPERTIES
TITLE OF INVENTION: DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 28205
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific TITLE OF INVENTION: Genes and Proteins PILE REFERENCE: DEX OFFICE OFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.6%; Score 20; DB 15; Length 698; Best Local Similarity 82.1%; Pred. No. 20; Matches 23; Conservative 0; Mismatches 5; Indels
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                                                             Sequence 102, Application US/10074475
Publication No. US20030092898A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Nu, Fing
APPLICANT: Karra, Kalpana
APPLICANT: Karra, Kalpana
APPLICANT: Cafferey, Recipon, Herve
APPLICANT: Cafferey, Robert
APPLICANT: Calferey, Robert
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
US-10-369-493-30964/c
; Sequence 30964, Application US/10369493
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US-10-369-493-28205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
GRGANISM: Homo sapien
US-10-074-475-102
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tobaska, Jack B
APPLICANT: Soloton Nouses Tobaska B
CURRENT APPLICATION NOUSES: 104/146
CURRENT PILING DATE: 2003-04-28
NUMBER P SEQ ID NOS: 73128
LENOTH: 2581
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 453;
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1 OTHER INFORMATION: Clone ID: PAT MRT3847 16816C.1
US-10-424-599-50726
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OTHER INFORMATION: Clone ID: UC-ZMFLB73059H03_FLIUS-10-425-114-30662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ATCTCTTCTCCGAGCCGGTCGAAATAGTGAG 32
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Patent No. US20020102731A1
GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Siv
APPLICANT: Sandalon, Siv
APPLICANT: Gnacenco, Dmitri
ITINE OF INVENTION: Adenoviral Vectors
ITINE REPERRICE: STONYB-04970
CURRENT FILING DATE: 2001-02-12
FRIOX PLICATION NUMBER: 60/337,747
FRIOX PLICATION NUMBER: 60/337,747
FRIOX PLICATION NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
ILENGTH: 34214
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 19.8; Dest Local Similarity 77.4%; Pred. No. 23; Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30662, Application US/10425114 Publication No. US20040034888A1 GENERAL INPORMATION:
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                          CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 50726
LENGTH: 453
                                                                                                                                                                                       TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPB: DNA ORGANISM: Zea mays
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Show Tihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5322)8
CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Resental, Andre
APPLICANT Preiberg, Christoph
APPLICANT Preiberg, Christoph
APPLICANT Perret, Xavier Philippe
APPLICANT Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPOGS
FILE REFERENCE: 2001-08-27
FILE REFERENCE: 2001-08-27
FILE REFERENCE: CARPOGS
FILE REFERENCE: CARPOGS
FILE REFERENCE: 2001-08-27
FILE REFERENCE: CARPOGS
FILE RE
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongahing
APPLICANT: Sun, Yongahing
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Genes and Proteins
TITLE OF INVENTION: Genes and Proteins
CURRENT APPLICATION NUMBER: US.1D/074,475
CURRENT PILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 295
SOFTWARE PARENT PILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
LENGTH: 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
60.6%; Score 20; DB 15; Length 1217;
Best Local Similarity 82.1%; Pred. No. 21;
Matches 23; Conservative 0; Mismatches 5; Indels
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Publication No. US20030054522Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p TYPE: DNA
j ORGANISM: Homo sapien
US-10-074-475-103
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ORGANISM: Rhizobium
US-09-939-964-1
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Sequence 4311, Application US/09796692

Sequence 4311, Application US/09796692

Publication No. US2002019836241

GENERAL INFORMATION:
APPLICANT GHIGGE, Paul A.
APPLICANT GHIGGE, Paul A.
APPLICANT Hannion, Jane
ITILE OF INVENTION: LOCREOSTITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
ITILE OF INVENTION: USCOPPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
ITILE OF INVENTION: UNRER: US/09/796,692
CURRENT FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (4187715)

OTHER INPORMATION: a, t, c, g, other or unknown UG-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CATCTCTCCGAGCCGGTCGAAATAGTGAG 32
                                                                                                                                                                                                                                   APPLICANT: SHIBA, TANAVOSHI
APPLICANT: SHIBA, TANAVOSHI
APPLICANT: SHIBA, TANAVOSHI
TITLE OF INVENTICAN: NOSHITRA
TITLE OF INVENTICAN: NOVEL POLYNCLEOTIDES
FILE REFERENCE: 249-262
CURRENT PLILNG DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JF 2001-204689
PRIOR PLILNG DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
ROWBER OF SEQ ID NOS: 15109
SEQ ID NO 1 SEQ ID NOS: 15109
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FILING DATE: 2000-05-22
APPLICATION NUMBER: 60/218,950
FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                CMURA, SATOSHI
INEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                   Sequence 1, Application US/1015
Publication No. US20030119018A1
GENERAL INFORMATION:
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US-09-796-692-4311/c
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                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                         Publication No. US2030215810A1

CENERAL INPORMATION NO. US2030215810A1

GENERAL INPORMATION NO. US2030215810A1

APPLICANT: LU, YI

APPLICANT: LU, YI

APPLICANT: LU, YI

APPLICANT: LO, YI

APPLICANT: COLOR CHANGES

FILE REPRENCE: 9800240-0019

CORREST APPLICATION NUMBER: US/10/144,679

CORREST APPLICATION NUMBER: US/10/144,679

CORREST APPLICANT: 2002-05-10

SOFTWARE: PATENTIN VOT: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INPORMATION: Description of Artificial Sequence: Synthetic CTHER INPORMATION: Zn-DNA US-10-144-679-14
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                                                                     Ouery March 58.8%; Score 19.4; DB 9; Length 34214; Best Local Similarity 79.3%; Pred. No. 59; Marches 23; Conservative 0; Mismatches 6; Indels 0;
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OTHER INFORMATION: Description of Artificial Sequence: Zn-DNA
US-10-144-094-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 50;
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Publication No. US20040023216A1
GREERAL INFORMATION:
APPLICANT: LIU, XI
APPLICANT: LIU, XI
APPLICANT: LIU, XI
CURRENT APPLICANT: LIU, YI
STILB REFERENCE: 10322/44
CURRENT APPLICANT: 2002-05-10
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 50
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                                                                                                                                                                                                                     12904 ATTITITICGGGCCGGTCGCAATAGGG 12876
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Pred. No. 35;
O; Mismatches
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Best Local Similarity 75.0%; Pred. No. 35;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                         2 ATCTCTTCTCCGAGCCGGTCGAAATAGTG 30
) ORGANISM: Human adenovirus type 40
US-09-782-378A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 75.0%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                RESULT 25
US-10-144-679-14
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US-10-144-094-14
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   Length 9025608;
                                                      Indels
Query Match 58.2%; Score 19.2; DB 15; Best Local Similarity 75.0%; Pred. No. 1.2e+02; Matches 24; Conservative 0; Mismatches 8;
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us-10-144-679-1.rmpb

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION WINDERS: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION WINDER: 60/223,378
; PRIOR PILING DATE: 2000-08-07
; SOUTWARE: PASEURG for Windows Version 3.0
; SEQ ID NO 4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATION: (71)

SR INFORMATION: n=A,T,C or G
B/KEY: unsure
B/KEY: unsure
B/KEY: unsure
BATION: (115)
BR INFORMATION: n=A,T,C or G
BATION: (115)
BR INFORMATION: n=A,T,C or G
BR INFORMATION: n=A,T,C or G
B/KEY: unsure
                                                                                                                                                                                                                                                                                                    ATION: (34)

RR INFORMATION: n=A,T,C or G
ATION: (36)

RR INFORMATION: n=A,T,C or G
BY KRY: unaure
ATION: (46)
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NAME/KET: unsurre
LOCHER INFORMATION: n=A,T,C or G
OTHER INFORMATION: n=A,T,C or G
LOCHER INFORMATION: n=A,T,C or G
NAME/KET: unsurre
LOCATION: (178)
OTHER INFORMATION: n=A,T,C or G
NAME/KET: unsure
LOCATION: (184)
NAME/KET: unsure
LOCATION: (192)
                                                                                                                                                                                                                            NAMB/KEY: ungure
LOCATION: (31)
OTHER INPGRMATION: n=A,T,C or G
NAMB/KEY: ungure
LOCATION: (34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEY: unsure
ION: (69)
INPORMATION: n=A,T,C or G
KEY: unsure
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INPORMATION: n=A,T,C or G
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MANE/KEY: UNBUILD
LOCATION: (146)
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NAME/KEY: unmenre
LOCATION: (221)
OTHER INFORMATION: n.A.T, C or G
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INFORMATION: n=A, T, C or G
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INPORMATION: n=A, T, C or G
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OTHER INFORMATION: n=A,T,C or G
NAME/KBY: unsure
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INFORMATION: n=A, T, C or G
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Gaiget, Alexander
APPLICANT: Adgiget, Alexander
APPLICANT: Adgiget, Narc
APPLICANT: Aggiget, Narc
APPLICANT: Aggiget, Narc
APPLICANT: Better, Narc
APPLICANT: Corita Corporation
APPLICANTON HUMBER: U300-11-06
APPLICANTON NUMBER: U300-11-06
APPLICANTON NUMBER: U300-11-06
APPLICANTON NUMBER: U300-3-17
APPLICANTON NUMBER: U300-3-14
APPLICANTON NUMBER: U300-
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PRIOR PLILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
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: Sequence 4311, Application US/10040862

: Publication No. US20030078396A1

: GENERAL INFORMATION:
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JOCATION: (385)
JOCATION: (413)
JOCATION: (413)
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NAME/KEY: unmeure
LOCATION: (317)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unmeure
LOCATION: (385)
INFORMATION: n=A, T, C or G
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SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 4311
LENGTH: 444
                                                                                                                                                                                                                                        NAME/KEY: ungure
LOCATION: (36)
THER INPORMATION: n=A,T,C or G
                                                                                                                     LOCATION: (31)
OTHER INFORMATION: n=A,T,C or 3
                                                                                                                                                                                                                                                                                                           NAME/KEY: unsure
COCATION: (46)
THER INFORMATION: n=A,T,C or G
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CCCATION: {64}
YHER INPORMATION: n=A,T,C or G
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LOCATION: (221)
OTHER INFORMATION: n=A,T,C or G
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'AMB/REY: unsure
CCATION: (69)
TTHER INFORMATION: n=A, T, C or G
'RATURE:
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INFORMATION: n=A,T,C or G
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INFORMATION: n=A,T,C or G
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THER INPORMATION: n=A,T,C or G
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THER INFORMATION: n=A,T,C or G
RATURE:
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CON: (146)
INFORMATION: n=A,T,C or G
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OCATION: (178)
THER INPORMATION: n=A, T,C or G
EATURE:
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INPORMATION: n=A,T,C or G
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THER INPORMATION: n=A,T,C or G
WARTURE:
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OCCATION: (184)
THER INFORMATION: n=A,T,C or
RATURE:
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INFORMATION: n=A,T,C or
                                                     TYPE: DNA
ORGANISM: Homo sapiens
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AMB/KBY: unsure
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PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: US 60/190,479

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APPLICAT: LU, YI
APPLICAT: LU, YI
APPLICAT: LU, YI
TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON
TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON
TITLE OF INVENTION: COLOR CHANGES
FILE REFERENCE: 9800240-0019
CURRENT PLILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 88
SOFTRARE: PATENTIN Ver. 2.1
LENGTH: 51
           PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEG ID NOS: 11290
SOTEWARE: PastSEG for Windows Version 3.0
LENGTH: 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.6%; Score 19; DB 16; Length 444; Best Local Similarity 78.6%; Pred. No. 56; Matches 22; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
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Best Local Similarity 76.7%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
| LOCATION: (1)...(444)
| CTHER INPORMATION: n = g, a, c or t
| U8-10-154-8848-4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/10144679
Publication No. US20030215810A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FRATURE:
                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20040005561A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Adjact, Paul A.
APPLICANT: Manion, Jane
APPLICANT: Retier, Marc W.
APPLICANT: Retier, Marc W.
APPLICANT: Retier, Marc W.
APPLICANT: Corixa Coxpositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REPERENCE: 014008-013521US
CURRENT APPLICATION NOTE:
UNERRY APPLICATION NOTE:
UNERRY PILING DATE.
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-03
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PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
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JICATION NUMBER: US 60/186,126
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PRIOR FILING DATE: 2000-05-04
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| DOCNTON: (1)...(444)
| OCHER INPORMATION: n = g, a, c or t
US-10-057-4758-4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-154-884B-4311/c
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                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE Patentin version 3.1
SEQ ID NO 14316
LENGTH: 846
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                             indels
    Best Local Similarity 76,7%; Fred. No. 71; Matches 23; Conservative 0; Mismatches
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                                                                    3 TCTCTTCTCCGAGCCGGTCGAAATAGTGAG 32
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Publication No. U820040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR PILLING DATE: 2000-03-20
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-03-21
PRIOR PILLING DATE: 2000-03-23
PRIOR PILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR PILLING DATE: 2000-05-66
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-01-02-33
PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-10-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-16
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Publication No. US20040034888A1
GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         carr, Grant
T: Yamamoto, Robert
i: Porsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Burkholderia mallei
US-10-282-122A-14316
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US-10-424-599-74527
US-10-424-599-74527
Sequence 74527, Application US/10424599
Publication No. US2004003107241
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Kovalic David K
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement PILIS REFERENCE: 38-21(53223)B
CURRENT APPLICANT: ON UNDER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 220
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J OTHER INFORMATION: Description of Artificial Sequence: 2n-DNA
US-10-144-094-17
                                                                  Length 51,
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                                                               DB 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PRATURE:

) OTHER INFORMATION: Clone ID: PAT_MRT3847_38311C.1

05-10-445-599-74527
                                                               Query Match 57.0%; Score 18.8; D
Best Local Similarity 76.7%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches
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Best Local Similarity 76.7%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches
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i LOCATION: (1):..(495)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5654
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ORGANISM: Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPB: DNA
ORGANISM: Glycine max
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APPLICANT: Yanghunco, Robert
APPLICANT: Yanghunco, Robert
APPLICANT: Yorsyth, R.
APPLICANT: Yorsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of EBBential Genes in Microorganisms
FILE OF INVENTION: Identification of EBBential Genes in Microorganisms
FILE OF INVENTION: MURBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
FRICK PILING DATE: 2000-03-21
FRICK PILING DATE: 2000-05-23
FRICK FILING DATE: 2000-05-23
FRICK FILING DATE: 2000-05-26
FRICK FILING DATE: 2000-05-06
FRICK FILING DATE: 2000-05-06
FRICK FILING DATE: 2000-05-06
FRICK FILING DATE: 2000-05-06
FRICK FILING DATE: 2000-01-03
FRICK FILING DATE: 2000-10-23
FRICK FILING DATE: 2000-11-27
FRICK FILING DATE: 2000-12-22
FRICK FILING DATE: 2000-12-24
FRICK FILING DATE: 2001-02-06
FRICK FILING DATE: 2001-02-
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Publication No. US20020172976A1
GENERAL INFORMATION:
APPLICANT: ROSG, Bride Carter
AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
CITY: PALO ALTO
CITY: CALO ALTO
CITY: CALO ALTO
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COMPUTER READABLE FORM:
MCDIUM TYPE: Diskette
COMPUTER: INS COMPATIBLE
OPERATING SYSTEM: Windows
SOFTWARE: PREISEQ for Windows
VOLUMENTER: PREISEQ for Windows
SOFTWARE: PREISEQ for WINDOWS
SOF
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Best Local Similarity 90.9%; Pred. No. 80;
Natches 20; Conservative 0; Mismatches
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APPLICATION NUMBER: US/10/194,163
PILING DATE: 04-Nov-2002
CLABSIPICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 ATCTCTCCGGGCCGGCCG 401
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; ORGANISM: Burkholderia mallei
US-10-282-122A-14254
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US-10-194-163-1029/c
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| Publication No. U520040034688A1 |
| GENERAL INPORMATION |
| APPLICANT: Liu, Jingdong |
| APPLICANT: Liu, Jingdong |
| APPLICANT: Chou, Yibua |
| APPLICANT: Rowals, David K. |
| APPLICANT: Cao, Yeven B |
| APPLICANT: Tabaska, Jack B |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa |
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| TITLE OF INVENTION: Nucleic Acid Molecules Associa |
| TITLE OF INVENTION: Nucleic Acid Molecules Associa |
| TITLE ACID MOLECULES |
| TITLE 
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Best Local Similarity 76.7%; Pred. No. 78;
Matches 23; Conservative 0; Mismatches 7; Indels C;
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57.0%; Score 18.8; DB 13; Length 1229;
Best Local Similarity 76.7%; Pred. No. 79;
Matches 23; Conservative 0; Mismatches 7; Indels 0;
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B.
APPLICANT: Tabaska, Jack B.
APPLICANT: Tabaska, Jack B.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for P.
TITLE OF INVENTION: Plants and Uses Thereof for P.
FILE REFERENCE: 38-21(53313) B.
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 25452
LENOTH: 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Triticum aestivum
; PEATUNE;
; PEATUNE; OTHER INFORMATION: Clone ID: LIB3910-027-D8_FLI
US-10-425-114-25452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PERTURE:
1 OTHER INPORMATION: Clone ID: LIB3399-014-A6_FLI
US-00-455-114-22309
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Gaps

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Query Match 57.0%; Score 18.8; DB 13; Length 3182; Best Local Similarity 76.7%; Pred. No. 87; Matches 23; Conservative 0; Mismatches 7; Indels 0;
      NAME: Bagu, Shantanu

REGISTRATION NUMBER: 43,318

REGISTRATION NUMBER: 529282000101

TELECOMONICATION INPORMATION:
TELEPHONE: 650-813-5995
TELEPHONE: 706141
INPORMATION POR SEG ID NO: 1029
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNROWN
ORIGINAL SOURCE: ORPHYROMONAS GINGIVALIS
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KBY: misc feature

LOCATION: 1...3182

SEQUENCE DESCRIPTION: 8EQ 1D NO: 1029

US-10-194-163-1029
ATTORNEY/AGENT INPORMATION,
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Search completed: May 24, 2004, 13:45:29 Job time : 216.245 secs

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Gaps õ

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

May 24, 2004, 07:43:51; Search time 202.981 Seconds (without alignments) 690.658 Million cell updates/sec Run on:

US-10-144-679-1

33
1 catctctcccgagccggtcgaatagtgagt 33 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 104 Maximum Match 1004 Licting first 45 summaries

N Geneseq 29Jan04: Database :

genesequi990s: • genesequ2000s: • genesequ2001as: • genesequ2001bs: • geneseqn2002s:* geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aal45459 RNA-cleav				6			Aah88480 CNS disor	Aal47338 Human GAB		Adc03463 Wheat flo		Human		Abt07624 Human bre	Continuation (5 of	Continuation (5 of	Aac40134 Arabidops			Abl30213 Drosophil	~	
SUMMARIES	;	a	AAL45459	AAL45380	AAL45398	AAL45397	AAL45396	AAL45399	AAL45386	AAH88480	AAL47338	AAQ37966	ADC03463	ADD48766	ABT 07623	ABK74026	ABTC7624	AAV30458 4	AAV30459_4	AAC40134	ABS69905	AAL45392	ABL30213	ABL30212	AAX88481
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Aa145395 Zinc-depe	Abk78363 Bacillus		Ada49038 Wheat ger	Adc03443 Wheat flo	-	-	_			-		_	Abx66285 Helicobac	Abx65642 Helicobac	Abx66280 Helicobac	Aax14487 H. pylori	Abk73388 Bacillus	Abr13569 Arabidop			AadC0943 Arabidops
AAL45395	ABX78363	AAX20782	ADA49038	ADC03443	ACA26446	ACA26384	ABQ61114	AAL45394	AAL45393	AAL45419	ABK16034	ADB95297	ABX66285	ABX65642	ABX66280	AAX14487	ABK73388	ABZ13569	ACA68024	AAE00944	AAD00943
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57.0	57.0	57.0	57.0	57.0	57.0	57.0	57.0	56.4	56.4	56.4	56.4	56.4	\$6.4	56.4	56.4	56.4	56.4	56.4	56.4	\$6.4	56.4
18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6
7	52	56	22	58	53	30	걸	32	33	34	32	36	37	38	39	9	7	7	Ţ	44	45
74	52	56	c 23	58	33	30	검	32	33	34	35	36	37	38	39	9	7	7	Ţ	44	•

ALIGNMENTS

/*tag= a
/*tag= a
//bound_molety= "substrate"
//note= "binds nucleotides 20-12 of the substrate shown in AAL45460" 11. 19
//rag= b
/*tag= c
/bound moiety= "substrate"
Abound moiety= "substrate"
AAL45460* Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; ribozyme; ss. Location/Qualifiers AAL45459 standard; DNA; 33 BP. RNA-cleaving deoxyribozyme #7. 06-JUN-2002 (first entry) Key misc_binding Unidentified. misc_binding AAL45459; stem_loop RESULT 1 AAL45459

WO20020006-A2. 03-JAN-2002.

27-JUN-2001; 2001WO-US020557.

27-JUN-2000; 2000US-00605558. (UNII) UNIV ILLINOIS FOUND.

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WPI; 2002-130823/17.

New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.

us-10-144-679-1.rng

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                                                                              The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quancher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
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/bound_moiety= "substrate 17D8"
/note= "binds nucleotides 9-1 of substrate 17ES shown in
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in AA445381"
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 33; DB 6; Length 33; 100.0%; Pred. No. 4.3e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                             Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 U; 0 Other;
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                              Example 1; Pig 6; 57pp; English.
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nes 33; Conservative
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substrate; ss.
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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is substrate of a ribozyme which may be used as a biosensor of the invention
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                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.04; Score 33; DB 6; Length 33; Local Similarity 100.04; Pred. No. 4.36-05; Main at Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 7 A; 9 C; 8 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATCITCTTCCGAGCCGGTCGAAATAGTGAGT 33
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Matchés 29; Concern
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AAL45397;

RESULT 4

AAL4539

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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                               New mucheic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26.4; DB 6; Length 50;
Pred. No. 0.044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50 BP; 14 A; 14 C; 11 G; 11 T; 0 U; 0 Other;
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96.4%; Pred. No. v..
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                                                                                                                                                                                                                                                                                                                                                    Example 1, Fig 2; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL45399 standard; DNA; 50 BP.
                                                           27-JUN-2001; 2001WO-US020557.
                                                                                                  27-JUN-2000; 2000US-0060558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-2001; 2001WO-US020557.
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                                                                                                                                         (UNII ) UNIV ILLINOIS POUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27, Conservative
                                                                                                                                                                                                                        WPI; 2002-130823/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130823/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200006-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                  Lu Y, Ci J;
                    03-JAM-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lu Y, Li J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to blosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The blosensors are useful for the sensitive and selective detection of ions. The blosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The blosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribosyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                           Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; ribozyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 26.4; DB 6; Length 50; 96.4%; Pred. No. 0.044; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50 BP; 13 A; 14 C; 11 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                    Zinc-dependent deoxyribozyme SEQ ID NO: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zinc-dependent deoxyribozyme SBQ ID NO: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 CTATTCTCCGAGCCGGTCGAAATAGTGA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CTCTTCTCCGAGCCGGTCGAATAGTGA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 2; 57pp; English.
                                                                           AAL45397 standard; DNA; 50 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL45396 standard, DNA, 50 BP
                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-2001; 2001WO-US020557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 96.4%;
es 27; Conservative
                                                                                                                                                           (first entry)
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                                                                                                                                                           06-JUN-2002
                                                                                                                                                                                                                                                                                                      Unidentified
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Lu Y,

AAL45396,

RESULT 5

AAL45396

Query Match

Best Loca Matches

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Gaps ö 1 CATCTCTTTTGTCAGCGACTCGAAATAGTGAGT 33

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                                                                 enryme dependent on an ion to produce a product, a quencher or/and a fluorophore and a phocodetector. The biosensors are useful for the senaitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribosyme which may be used as a biosensor of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 6; Length 50; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                         comprising
                                                                                                                                                                                                                                                                                                                                                             Sequence 50 BP; 12 A; 11 C; 10 G; 17 T; 0 U; 0 Ocher;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zn(II) -dependent trans-cleaving deoxyribozyme 1781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33 BP; 8 A; 7 C; 7 G; 11 T; 0 U; 0 Other;
                            present invention relates to biosensors,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.7%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.5 Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CITCTCCGAGCCGGTCGAAATAGT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CTTCTCCGAGCCGGTCGAAATAGT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL45386 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-2000; 2000US-00605558.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-JAN-2002
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AML45386
TO AML45386

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The present invention relates to biallelic markers derived from human genes involved in central nervous system (CMS) disorders. The present sequence is one such biallelic marker derived from human GABA-A receptor subunit (GABRG2) gene. GABA is gamma aminobutyric acid. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in a biological sample, where the markers comprise at least one CNS disorder related marker
                                                                                                                                                                                                                                                                                                                                   Single nucleotide polymorphism; SNP; biallelic marker; human; ds; central nervous system disorder; CNS; GABRG2; GABA-A receptor subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polymucleotides, useful for genotyping mucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker.
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/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                    CNS disorder-related biallelic marker #2 from GABRG2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human GABP beta-HSV1 VP16 fusion protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 475 BP; 137 A; 92 C; 98 G; 146 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TCTCTTCTCCGAGCCGGTCGAATAGT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 147; 519pp; English.
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                                                                      AAH88480 standard; DNA; 475 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2001; 2001WO-IB000116.
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                                                                                                                                                                                                         26-FBB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200151659-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001,
                                                                                                                                         AAH88480;
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BDT 26-P

BDT 26
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CATCTCTCCCGAGCCGGTCGAAATAGTGAGT 33

Best Loca Matches

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Sequence encoding purine-rich repeat (GA repeat) binding protien (GABP) subunit beta 1. GA binding protein; cis-regulatory element; VP16 mediated induction; as

Location/Qualifiers 133. .1281

Mus musculus

/*tag=

WO9304166-A1 04-MAR-1993.

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The present invention provides a nucleic acid capable of controlling the expression of a gene and being activated by an Bis-transcription factor (BLF) related compound. The nucleic acid is useful for screening and/or providing candidate compounds capable of regulating transcription. This is involves bringing the nucleic acid into contact with compounds to be corrected and desecting the transcriptional activity from the nucleic acid into contact with compounds to be contained and detecting the transcriptional activity from the nucleic and/or synchesising the positively tested compound. A construct of containing the sequence of the oppound and optionally purifying and/or synchesising the positively tested compound. A construct of containing the sequence is useful for activating the expression of a gene containing the sequence is useful for activating the expression of a containing the control, such as the utrophin gene, interleukin (IL)-2 gene, acetylcholine receptor (AchR) delta and epsilon submits gene or acetylcholine receptor (AchR) delta and epsilon submits genes, for the treatment of muscle diseases, preferably Duchenne or Becker muscular sequence is the coding sequence of a fusion protein of the human GABP containing type I VP16
Human; utrophin B; promoter; Bts-transcription factor; transactivator; muscular distributar distributar distributar distributar distributar distributar gene therapy; muscle wasting; cytostatic; immunostimulant; haemostatic; haemophilis; immune deficiency; cancer; HSVI, VP16; GABP bets; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid capable of controlling the expression of a gene and being activated by an Ets-transcription factor related compound, useful for screening candidate compounds capable of regulating transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1248 BP; 336 A; 285 C; 340 G; 287 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                             /*tag= a.
/product= "GABPbeta_VP16 fusion protein"
                                                                                                                                                                                                                           Location/Qualifiers
1. .1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 2D; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MYOC-) MYOCONTRACT PHARM RES AG.
                                                                                                                                                Herpes simplex virus; type 1. Synthetic. Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2001; 2001WO-EP012662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-2000; 2000EP-00123842
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Best Local Similarity 85...
Best Local Similarity 85...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-500123/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAO18052
                                                                                     fusion protein.
                                                                                                                                                                                                                                                                                                                                             WO200236620-A2.
                                                                                                                                 Homo sapiens.
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ADC03463 standard, DNA, 1254 BP.
                                                                                                                                                               18-DEC-2003 (first entry)
                      23, Conservative
Query Match
Best Local Similarity
                                                                                                                                           ADC03463;
            Best Locz
Matches
                                                                                                RESULT 11
                                                                                                            ADC03463
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                                                            62.4%; Score 20.6; DB 6; Length 1248; 85.2%; Pred. No. 30; 11ve 0; Mismarches 4; Indels 0;
                                                                                                                    168 TCTTCTCCGAGCCGGTGTAAGTAGAGA 194
                                                                                                      5 TCTTCTCCGAGCCGGTCGAATAGTGA 31
                                                                                                                                                                               AAQ37966 standard, cDNA, 2616
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(revised) (first entry)

25-MAR-2003 AAQ37966,

SAKKE

RESULT 10 AAQ37966

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Gaps
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                                                            62.4%; Score 20.6; DB 2; Length 2616; 85.2%; Pred. No. 34; cive 0; Mismatches 4; Indels 0.
Sequence 2616 BP; 742 A; 557 C; 593 G; 724 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wheat flowering time-related DNA sequence #23.
                                                                                                                                                                                                                                300 TCTTCTCCGAGCCGGTGTAAGTAGAGA 326
                                                                                                                                                                                 S TCTTCTCCGAGCCGGTCGAAATAGTCA 31
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A cis-regulatory element required for virion associated protein VP16 madiated induction of herpes simplex virus 1 (HSV1) immediate early (IE) genes consists of three imperfect repeats of the purine-rich interaction of the imperfect repeats of the purine-rich interaction with the purine-rich repeats of xepeats) has been identified in soluble preparations of rat liver nucleif. This GA binding protein (GAB) consists of two separable schunits. Applicants have isolated CDNA clones encoding both subunits of GABP and have revealed that one (GABP alpha) is related to the Ets transforming protein, while the other (GABP obeta) contains a series of 33-amino acid repeats related in sequence to variety of proteins. The sequences for GABP-beta-1 and GABP-beta-2 are identical up to nucleotide lillo except for a three nuclaocide innertion (GTA) at posm. 828 of GABP-beta-1. (Updated on 25-MAR-2003 to correct PN

(GTA) at posn. 828 of GABP-beta-1. (Updated on 25-MAR field.) (Updated on 25-WAR-2003 to correct PI field.)

DNA encoding GA binding protein sub-unit - allows investigation of sub-unit sequence motif functions, for control of rapid cell division e.g. in cancer.

Claim 7, Fig 2B1-3, 68pp; English.

Mcknight SL, Thompson CC, Lamarco KL,

WPI; 1993-093998/11.

P-PSDB; AAR33366.

(CARN-) CARNEGIB INST WASHINGTON.

92WO-US006748. 91US-00746032.

17-AUG-1992;

16-AUG-1991;

us-10-144-679-1.rng

03-JAN-2003

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also chaimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a differentially expressed in neuronal tissue of a first animal that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition of activity in an animal of one or more of the polypeptides or their animal of one or more of the polypeptides or their animal composition comprishing the one or more of polypeptides or their animal composition comprishing the one or more of polypeptides or their animal composition comprishing the one or more of the polypeptides or their animal composition comprishing the one or more of the parameterization which encodes one of the polypeptides of the invention that the appendence presented during pain. Note: The sequence data for this patent did not form part of the printed specification, but was for the printed specification, but which is differentially expressed during pain. Note: The sequence data for the printed specification, but which is differentially expressed during pain. Note: The sequence during pain or the sequence data for the printed specification, but which is differentially expressed during pain.
                                                                                       New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; breast specific gene; breast specific protein; breast cancer; gene therapy; cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer associated coding sequence SEQ ID NO: 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 61.2%; Score 20.2; DB 9; Length 2695; Best Local Similarity 75.8%; Pred. No. 52; Matches 25; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2695 BP; 772 A; 574 C; 656 G; 693 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wfpo.int/pub/published_pct_sequences.
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ABT07623 standard; cDNA, 698 BP.
                                                                                                                                                           Claim 1, Page; 1017pp; English.
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                      WPI; 2003-268312/26.
GENBANK; 875037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises the amino acid and coding sequences of proteins involved in the control of flowering time in rice. The DNA and protein sequences of the invention are useful for modulating flower architecture and flowering time, the DNA and protein sequences are useful in the area of plant biotechnology, commercial plant farming and agriculture. The present wheat DNA sequence shows homology to the rice sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a polypeptide modulating flower architecture and flowering time, useful in the area of plant biotechnology, and commercial plant farming and agriculture.
                                                                                                                                                                                                                                                                                                                 Zhu T;
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1254 BP; 301 A; 296 C; 335 G; 322 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
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80.0%; Pred. No. 37;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 103, 323pp; English
                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 875037, 8EQ ID NO 14476.
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26-SEP-2001, 2001US-0335277P.
30-NOV-2001, 2001US-0334984P.
                                                                                                      24-JUN-2002, 2002WO-EP006968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0 les 24, Conservative
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                 WO2003000904-A2.
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Query Match

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1 CATCTCTCCCGAGCCGGTCGAATAG 28
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                                                                                                                                                                                                                                                                      Claim 1; Page 226; 367pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK74026 standard; DNA; 1018 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 60.6%;
Local Similarity 82.1%;
Nes 23; Conservative 0
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27-MAR-2001; 2001US-0279526P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                        Salceda S, Macina RA,
Sun Y, Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
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                                                                                                      WPI; 2002-657582/70.
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Best Local S
Matches 23
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XX ABK74

XX ABK74

XX ABK74

XX ABK74

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YX BAC10

XX BAC11

XX BAC1

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a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or acres second Bacillus cells. The method is useful for monitoring Global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring danages in expression of genes may be used to provide a representation of the way in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, or up characterisation is unnecessary, when one spot on an array equals one control or or one open reading frame, since sequence information is available. This sequence represents a genomic sequence did not form to the firwention. Note: The sequence data for this patent did not form to part of the printed specification, but was obtained in electronic format verver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, breast specific gene, breast specific protein, breast cancer, gene therapy, cytostatic, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast cancer associated coding sequence SEQ ID NO: 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 60.64; Score 20; DB 6; Length 1018; 1 Similarity 82.11; Pred. No. 54; 23; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1018 BP; 328 A; 207 C; 266 G; 217 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATCICITCTCCGAGCCGGTCGAATAGE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                845 ATGACTTCCCGTGGCGTCGAAATAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                           The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosts and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GBI), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of
                                                                                                                                                  New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therepy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
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                                  Cafferkey R;
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Pred. No. 51;
0; Mismatches 5; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 698 BP; 205 A; 126 C; 161 G; 206 T; 0 U; 0 Other;
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                               Karra K,
                               Hu P, Recipon H,
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Gape

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5; Indels

6; Length 1217;

Score 20; DB 6 Pred. No. 56; 0; Mismatches

Query Match
Best Local Similarity 82.1%;
Matches 23; Conservative

Sequence 1217 BP; 385 A; 210 C; 277 G; 345 T; 0 U; 0 Other;

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Gaps

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99U8-0125788P.
99U8-0126264P.
99U8-0126234P.
99U8-0128234P.
99U8-0128234P.
99U8-0128234P.
99U8-0139845P.
99U8-0130649P.
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9908-0134768P-
9908-0134941P-
9908-0135124P-
9908-0135353P-
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99US-0134218P.
99US-0134219P.
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9905-0139459P
9905-0139461P
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9905-0139453P
9905-0139750P
9905-0139750P
9905-0139899P
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990S-0140354P.
990S-0140695P.
990S-0140823P.
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23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
119-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
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22 - 70N - 1999;
23 - 70N - 1999;
24 - 70N - 1999;
26 - 70N - 1999;
29 - 70N - 1999;
30 - 70N - 1999;
01 - 70N - 1999;
01 - 70N - 1999;
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8-JUN-1999;
8-JUN-1999;
  AAV30459 4
Continuation (S of 6) of AAV30459 from base 400001 (Rhizobium species symbictic plasmid Continuation (S of 6) of AAV30459 from base 400001 (Rhizobium species symbictic plasmid WP Sequence split into 6 fragments LOCUS AAV30459 Accession Aav30459 WP AAV30459 0 100001 110000 WP AAV30459 2 200001 310000 WP AAV30459 3 300001 310000 WP AAV30459 5 500001 536165
                                                            RESULT 16
AAV30458 4
Continuation (5 of 6) of AAV30458 from base 400001 (Rhizobium species plasmid pNGR234a.)
HP Sequence split into 6 fragments LOCUS AAV30458 Accession Aav30458
HP Pragment Name Begin End
HP AAV30458 0 100001 210000
HP AAV30458 200001 310000
HP AAV30458 4 400001 510000
HP AAV30458 5 500001 510000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
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                                                                                                                                                                                  Score 20; DB 2; Length 110000;
Fred. No. 1.1e+02;
0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                 Query March 60.6%; Score 20; DB 2; Length 110000; Best Local Similarity 82.1%; Pred. No. 1.18+02; Matches 23; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana nNA fragment SEQ ID NO: 27179.
                                                                                                                                                                                                                                        55880 CICTICACCGAGCCGGTCGACCTGCTGA 55907
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS880 CTCTTCACCGAGCCGGTCGACCTGCTGA 55907
           1 CATCTTTTCTCCGAGCCGGTCGAAATAG 28
                                                                                                                                                                                                                           4 CICTICICOGAGCCOGICGAAIAGIGA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CTCTTCTCCGAGCCGGTCGAATAGTGA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC40134 standard; DNA; 1230 BP
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99U8-0123180P.
99US-0123548P.
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                                                                                                                                                                                  Ouery Match
Best Local Similarity 82,1%;
Matches 23; Conservative
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05-MAR-1999;
09-MAR-1999;
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HR 16-JUL-1999 9918-0144085 PR 119-JUL-1999 9918-01444131 PR 119-JUL-1999 9918-01446132 PR 119-JUL-1999 9918-01446132 PR 119-JUL-1999 9918-0144614 PR 119-JUL-1999 9918-0146146 PR 119-JUL-1999 9918-0146146 PR 119-JUL-1999 9918-0146146 PR 119-JUL-1999 9918-014614 PR 119-JUL-1999 9918-01461 PR 119-J
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Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor; adenovirus; adenovirus; severe combined irmune deficiency; PAH; beta-chain; heemoglobin gene, beta-thalassemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; blosphortolesterolaemia; bhypoxanthine-guanine phosphortoleyltransferase; lesch-Myhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylectonuria; dystrophin gene; muscular dystrophy; cystic fibrosis transmembrane conductance regularor gene; antilipaemia; antilipaemia; noorropic; cytostatic; dermatological; human adenovirus genome; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   32
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8est Local Similarity 75.0%; Pred. No. 69;
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adenovirus type 40 genome sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS69905 standard, DNA, 34214 BP
             12-PEB-2001; 2001US-00782378.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human adenovirus type 40.
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07-0CT-1999)

13-0CT-1999)

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26-0CT-1999
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The present invention relates to a new method of producing a vector. The method involves introducing recombinant vector having nucleotide sequence (18) having 5 and 3 end, left and right inversed terminal repeats of adenovirus lanking NS, adenovirus packaging sequence linked to inverted terminal repeat, and adeno-associated virus terminal repeat of inverted terminal repeat and adeno-associated virus terminal repeat linked to 3' end oil Luring cell to produce another vector. The method is useful for generating vectors applications (e.g. gene therest into a cell, for gene transferring nucleotide sequences of interest into a cell, for gene transferring nucleotide sequences of interest into a cell, for gene transferring nucleotide sequences of interest into a cell, for gene transferring sectored sequences are useful for treating diseases associated with it, i.e. adenosine deaminase gene associated with adenosine deaminase deficiency with severe combined immune deficiency, beta-chain of the medical phypercholesterolaemia, hypoxonthine-quanine themporibootyltransferase associated with Lessch-Nyhan syndroms, phenylalanine hydroxylase (PAR) gene associated with phenylatomuria, dystrophin gene associated with muscular dystrophy, and human cystic fibrosis transmenhrane conductance requence represents a human adenovirus genome sequence that was used in the methods of the invention
                                                                                                                                                       Producing vector, by introducing vector having nucleotide sequence, adenovirus inverted terminal repeats and packaging sequence, and adenoassociated virus terminal repeat, into cell, and culturing cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34214 BP; 8509 A; 8969 C; 8556 G; 8180 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.8%; Score 19.4; DB 6; Length 34214; 79.3%; Pred. No. 1.88+02; tive 0; Mismatches 6; Indele 0;
                           Gnatenko DV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12904 ATTTTTTCCGGCCGGTCGCATAGG 12876
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                                                                                                                                                                                                                                                                                                           Disclosure; Page 166-181; 191pp; English
                               Sandalon Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL45392 standard; DNA; 50 BP
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                                   Bahou WP,
                                                                                             WPI; 2002-690619/74.
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Local Si.
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                                   Hearing P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL45392,
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WPI; 2002-130823/17.

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                                                                                                                 The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophile. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiG176-ABLJ0511), expressed DNA sequences (ABLiG176-ABLJ0511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic formst directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                         Gaps
               New nucleic acid enzyme biosensors, useful for the sensitive and absective detection of ions, particularly metal ions e.g. lead ions, for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila, devalopmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genomic polymucleotide SEQ ID NO 42112.
                                                                                                                                                                                                                                                                                                               Score 19.2; DB 6; Length 50;
Pred. No. 78;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 42112; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                   Sequence 50 BP; 12 A; 10 C; 12 G; 16 T; 0 U; c Other;
                                                                                                                                                                                                                                                                                                                                                                                           2 ATCICITCICCGAGCCGGTCGAAATAGTGAGT 33
                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATCTCTTTTGTCAGGACTCGAAATAGTGTGT 32
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                                                                                     Example 1; Fig 2; 57pp; English.
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ABL30213 standard; DNA; 1512 BP.
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                                                                                                                                                                                                                                                                                                                     Query Match 58.2%;
Best Local Similarity 75.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI, 2001-656860/75.
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RESULT 22

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ABL3 021

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This invention describes novel oligonucleotides which are used for detecting the chemokines RANTES (regulated upon activation normal T expressed and secreted), macrophage inflammatory protein (MIP)-1 alpha or MIP-1 beta by (a) obtaining a sample possible containing RANTES or MIP-1 beta by (a) obtaining a sample possible containing RANTES or MIP-1 alpha or MIP-1 beta RAN, (b) performing an isothermal transcriptional amplification on the sample with 2 oligonucleotide primers, (c) detecting the product of step (b) where detection of a product indicates the product of RANTES MIP-1 alpha or MIP-1 beta in the sample. The assay is used to determine the levels of the chemokines RANTES, MIP-1 alpha and to be inhibitors of CO+ T-cells by primary non-syncytium-inducing HIV-1 to be inhibitors of CO+ T-cells by primary non-syncytium-inducing HIV-1 or stains. Thus the level of expression of these genes can be used as prognostic markers for direct therapeutic management of HIV-infected patients. By being isothermic, the assay requires less manipulation by the experimenter. Also 'spiking' the sample with a known amount of control RAN allowe quantitation and qualification of the products in a method of the invention
                                                                                                                                               RANTES; chemokine; detection; primer; probe; amplification; MIP-: alpha; regulated upon activation normal T expressed and secreted; MIP-1 beta; macrophage inflammatory protein; CD4 T-cell; inhibitor; prognosis; primary non-syncytium-inducing HIV-1 strain; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of expression levels of the cytokines RANTES, MIP-lalpha and MIP-lbeta used as prognostic markers of HIV-infected patients.
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                                                                                                        Human MIP-1 beta primer PlC*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00010641.
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                                                            (first entry)
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                                                                                                                                                                                                                                                            Synthetic.
                   AAX88481,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental blology and in elucidating cell signalling and inserecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABList76-ABList31), expressed DNA sequences (ABList76-ABList31), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genomic polymucleotide SEQ ID NO 42109.
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                   Sequence 1512 BP; 367 A; 403 C; 402 G; 340 T; 0 U; 0 Other;
                                                       Score 19; DB 4; Length 1512;
Pred, No. 1.6e+62;
0; Mismatches 5; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 4; Length 3686; Pred. No. 1.9e+02; 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, SEQ ID NO 42109, 21pp + Sequence Listing, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3686 BP; 993 A; 865 C; 837 G; 991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2602 CATTICTACTCCGAGCCGGTTAAATTA 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD, Myers EW;
                                                                                                                                                 1 CATCTCTCCGAGCCGGTCGAATA 27
                                                                                                                                                                                        CATTICTACICCAGCCGGTTAATTA S9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATCTCTCCCGAGCCGGTCGAAATA 27
                                                                                                                                                                                                                                                                                                   ABL30212 standard; DNA; 3686 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX88481/c
ID AAX88481 standard; DNA; 50 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                          Query Match 57.64;
Best Local Similarity 81.54;
Matches 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.54;
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 81.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drcsophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PRKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes from Dr
interactions.
                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photoderector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                             New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
              Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.0%; Score 18.8; DB 6; Length 51; Best Local Similarity 76.7%; Pred. No. 1.2e+02; Matches 23; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51 BP; 14 A; 10 C; 12 G; 15 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus clausii genomic sequence tag (GST) #1206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ATCTCTTCTCCGAGCCGGTCGAATAGTCA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAGTTCTACCAGGGTTCGAAATAGTGA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 2; 57pp; English.
                                                                                                                                              27-JUN-2001; 2001WO-US020557.
                                                                                                                                                                          27-JUN-2000; 2000US-00605558.
                                                                                                                                                                                                       (UNII ) UNIV ILLINOIS FOUND
                                                                                                                                                                                                                                                                 WPI; 2002-130823/17.
                                                                                    WO200200006-A2.
                                                      Unidentified.
                                                                                                                                                                                                                                      Li J;
                                                                                                                  3-JAN-2002,
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cells relative to expression of the genes in other Bacillus cells, comprising hybridiaing labelled nucleic acid probes is other Bacillus cells comprising hybridiaing labelled nucleic acid probes isolated from Bacillus cells con a substrate containing array of Bacillus general carray and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells. The method is useful for a spot in the array. The method is useful for conitoring can one or more second Bacillus cells. The method is useful for conitoring gene copy number variation and stability. Monitoring changes in one or more second Bacillus cells. The method is useful discovaring new genes; identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in which Bacillus cells adapt to changes in culture conditions, or which Bacillus cells adapt to changes in culture conditions, culture carriaction is unnecessary, when one spot and a rarray equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence timformation is available. This sequence represents a genomic sequence the partner of the printed specification, but was obtained in electronic formation is enter of the printed specification, but was obtained in electronic formation is recovery.
                                                                                                 Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treponema pallidum infection; syphilis; Borrella infection; animal; enzyme production; de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Match S7.0%; Score 18.8; DB 6; Length 495; Local Similarity 76.7%; Pred. No. 1.7e+02; es 23; Conservative 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 495 BP, 147 A, 103 C, 113 G, 111 T; 0 U; 21 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ICTCTTCTCCGAGCCGGTCGAATAGTGAG 32
                                                                                                                                                                                                     Claim 11; SEQ ID NO 5654; 200pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ICTCTTCTCCGAGCGCTTGCAAATAGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US013041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX20782/c
ID AAX20782 standard; DNA; 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1999 (first entry)
                  Clausen 1G,
                                                            WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-081273/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Praber CK;
                    Berka R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX20782;
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Score 18.8; DB 8; Pred. No. 1.8e+02; 0; Mismatches 7;

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Length 734;

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flowering time; wheat; flower architecture; plant blotechnology; commercial plant farming; agriculture; flowering-related protein; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Whear flowering time-related DNA sequence #3.
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                                                                                                              rerementedagecoarceananage 32
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                57.0%;
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26-SEP-2001; 2001UG-0325277P.
30-NOV-2001; 2001UG-0334984P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2002, 2002WO-EP006968.
                                                                                                                                                                                                                                                       ADC03443/c
ID ADC03443 stendard; DNA; 734
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                          1 Similarity 76.7 23.1 Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W02003000904-A2.
                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2003
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                  Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                  ADC03443,
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                  New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease registance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant;
                                                                                                                                                           AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, disgnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a movel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or colerance to a plant pathogen. The present sequence represents a gene conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Score 18.8; DB 2; Length 636;
Pred. No. 1.8e+02;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glazebrook J. Briggs S. Cooper B. Goff SA, Moughamer T. Katagiri F. Kreps J. Provart N. Ricke D. Zhu T.
                                                                                                                                                                                                                                                                                                                                  Sequence 636 BP; 175 A; 163 C; 136 G; 161 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wheat gene conferring disease resistance in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CACATCTCCCAGCTGGTCCAAGTAGTGGGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 1108; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CTCTTCTCCGAGCCGGTCGAAATAGTGAGT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                              Claim 1, Page 900; 1150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                             / Match 57.0%;
Local Similarity 76.7%;
les 21; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2002, 2002WO-IB002453.
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26-SEP-2001; 2001US-035227TP.
22-MAR-2002; 2002US-0366535P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038/c
ADA49038 standard; DNA; 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum.
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Matches
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Zhu T;

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                                                                                                                                                                                        The invention comprises the amino acid and coding sequences of proteins involved in the control of flowering time in rice. The DNA and protein sequences of the invention are useful for modulating flower architecture and flowering time, the DNA and protein sequences are useful in the area of plant biotechnology, commercial plant farming and agriculture. The present wheat DNA sequence shows homology to the rice sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
New isolated nucleic acid molecule encoding a polypeptide modulating
flower architecture and flowering time, useful in the area of plant
bloweethnology, and commercial plant farming and agriciture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.0%; Score 18.8; DB 9; Length 734; 76.7%; Pred, No. 1.8e+02; ive 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 734 BP; 166 A; 207 C; 222 G; 139 T; 3 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSS TOTOTOCACOGAGOCGGCCTAGAAAGTGGG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TCTCTTCTCCGAGCCGGTCGAATAGTGAG 32
                                                                                                                             Disclosure; SRQ ID NO 83, 323pp; English.
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ACA26446
ID ACA26
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AC ACA26
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761 Arcgcraccaccacccccccccccacaccaca 790
2 ATCTCTCCGAGCCGGTCGAAATAGTGA
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ACA26384 standard; DNA; 1371 BP

RESULT 3 ACA26384

19-JUN-2003 (First entry)

ACA26384;

21-MAR-2001; 2001US-00815242. 06-5BP-2001; 2001US-00948993. 25-CCT-2001; 2001UB-0142923P. 08-FBB-2002; 2002US-03672851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107 Burkholderia mallei. drug design; gene. W0200277183-A2. 03-OCT-2002.

Antisense; ds; prokaryotic essential gene; cell proliferation;

Prokaryotic essential gene #8103.

19-JUN-2003 (first entry)

Haselbeck R, Oblsen KL, Yamamoto R, Porsyth RA, Malone C, Carr GJ, (BLIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, Wang L, Wall D,

Syskind JW; Xu HH;

WPI; 2003-029926/02. P-PSDB; ABU22576.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SBQ ID NO 14316; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid ministry promoter operably linked to the mucleic acid.

(2) a vector comprising a promoter operably linked to the mucleic acid.

(3) an isolated of the fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of its fragment whose expression is inhibited by the activity of the polypeptide; (5) producting the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies pathway in which a proliferation-required gene or its gene product lies overawpressed; (7) antibition of an organism acts; (9) amanufacturing an antibion: (10) profiling the extent to which each of the strains as present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational dung discovery programs, or for screening for homologous mucleic acids required for proliferation in cells other. than S; aureus, S. typhimurium, C. prokaryotic sessential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in cells other and the sequence of an expansion of the printed specification; but was obtained in cells other the sequence of the printed specification.

Sequence 846 BP; 153 A; 286 C; 280 G; 127 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences

Gape ö / Match 57.0%; Score 18.8; DB 7; Length 846; Local Similarity 76.7%; Pred. No. 1.86+02; Sconservative 0; Mismatches 7; Indels Query Match Best Loc Matches

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Zyskind JW; Xu HH; Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene. Haselbeck R, Ohlsen KL, Yamamoto R, Forsych RA, Prokaryotic essential gene #8041. Malone C, Carr GJ, 21-WAR-2001; 2001US-00B15242. 66-SEP-2001; 2001US-0094B993. 25-OCT-2001; 2001US-0342921P. 08-FEB-2002; 2002US-00072851. 06-WAR-2002; 2002US-0362699P. 21-MAR-2002; 2002WO-US009107. (ELIT-) BLITRA PHARM INC. Zamudio C, Trawick JD, WPI; 2003-029926/02. P-PSDB; ABU22514. Burkholderia mallei WO200277183-A2. 03-OCT-2002, Wang L, Wall D,

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a prococer operably linked to the nucleic acid inhibites proliferation of the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide of its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of the polypeptide for proliferation, or that inhibits cellular proliferation of an activity a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiological proliferation of an organism acts; (9) manufacturing an antibiological proliferation of an organism and acts; (10) proliferation of an organism; or (11) identifying the target of a compound that inhibits the proliferation of an organism. The atrients of a compound that inhibits the proliferation of an organism. The arisense nucleic acids are useful for dentifying proteins or acreeming for homologous nucleic acids are useful for dentifying proteins or acreeming for homologous mucleic acids are sequired for proliferation in cells other than 8, aureus, 8, typhimutim, cequired for proliferation in cells other than 8, aureus, 8, typhimutim, 8, present than 8, aureus, 8, typhimutim, 8, present than 8, aureus, 8, typhimutim, 8, present than 8, aureus, 8, typhimutim, 8, the present sequence is one of the target Claim 14; SEQ ID NO 14254; 1766pp; English.

Length 1926;

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prokaryotic essential genes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from MIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides and their encoded proteins, useful as nutritional sources or supplements, or in gene therapy, particularly for treating wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuroprotective; immunomodulator; cancer; chromosome 17; cytostatic; anti-inflammatory; gene therapy; nutritional supplement; wound; burn; ulcer; Altriener's disease; Huntington's disease; amyotrophic lateral sclerosis; autoimmune disorder; inflammation; vulnerary; gene; ss.
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                                                                                                                                                                         / Match S7.0%; Score 18.8; DB 7; Length 1371; Local Similarity 90.9%; Pred. No. 2e+02; Onservative 0; Mismatches 2; Indels 0
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                                                                                                                              Sequence 1371 BP; 138 A; 496 C; 484 G; 253 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1, SEC ID # 327; 357pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C, Zhou P, Asundi V, Zhang J,
Xue AJ, Yang Y, Wehrman T, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLJ20123 fis clone encoding sequence.
                                                                                                                                                                                                                                                                                                                   380 ATCTCTTCACCGAGCCGGGCGA 401
                                                                                                                                                                                                                                                                                    2 ATCTCTTCTCCGAGCCGGTCGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ61114 standard; cDNA; 1926
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N-PSDB; ABP43870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nuclaic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
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                                                      Gaps
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/ Match 57.0%; Score 18.8; DB 6; Local Similarity 76.7%; Pred. No. 2.1e+02; tes 23; Conservative 0; Mismatches 7;
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This sequence represents a polynuclectide of the invention. It was isolated from Helicobacter pylori and encodes a h.pylori GHPO protein. The polyneptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and attrophic gastritis, and peptic ulter diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and
specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of protein holds the modulating compounds which bluds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This sequence encodes a selected interacting domain (SID), identified via protein-protein interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection, gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Helicobacter polynucleotides - used to develop products the diagnosis, prevention and treatment of Helicobacter infections an gastrointestinal diseases.
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                                                                                                                                       Match 56.4%; Score 18.6; DB 6; Length 1024; Local Similarity 84.0%; Pred. No. 2.3e+02; es 21; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                              Sequence 1024 BP; 267 A; 186 C; 240 G; 331 T; 3 U; 0 Other;
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                                                                                                                                                                                                                                  CATCTCTTCTCAAA 831
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97US-00881227.
97US-00902615.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHPO protein; Helicobacter
peptic ulcer disease; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori GHPO 1125 gene.
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24-JUN-1997;
29-JUL-1997;
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                                                                                                                                                                                                                           The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial procein may be used for treating or preventing ulcers in a human or animal. This sequence encodes a selected interacting domain (81D), identified via
                                                                                                                       New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing ulcers in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
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m i} gene, ds.
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Pred. No. 2.38+02;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1024 BP; 267 A; 186 C; 240 G; 331 T; 0 U; 0 Other;
                                                    Labigne A;
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                                                    De Reuse H,
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                                                    Colland F,
                                                                                                                                                                                                                                                                                                                                             protein-protein interactions
                                                                                                                                                                                                                                                                                                                                                                                                           Match 56.4%;
Local Similarity 84.0%;
Hes 21; Conservative
       (HYBR-) HYBRIGENICS. (INSP ) INST PASTEUR
                                                    Legrain P. Rain J.
                                                                                 WPI; 2002-674910/72.
P-PSDB; ABU50898.
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Matches
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셤 8

Best Local Similarity 84.04; Pred. No. 2.38+02; Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps

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Search completed: May 24, 2004, 11:14:44 Job time : 206.981 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model	:57 ; Search time 973.189 Seconds (without alignments) . 1469.725 Million cell updates/sec	-10-144-679-1 catetettetegageeggtegaaatagtgagt 33	1.0	21671516995 residues	sen parameters: 6940544		* Bummaries																						
nucleic search, using	(24, 2004, 10:18:57	US-10-144-679-1 33 1 catctcttctccgago	IDENTITY NUC Gapop 10.0 , Gapext	3470272 seqs, 2167	hits satisfying chosen parameters:	Jth: 0 Jth: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 s	GenEmbl:	95_58:	: #0 q6	gbpati	ge de la	gb_ro:•		99 4			# : # E E E E E E E E E E E E E E E E E			='E'		: em_un:• : em_vi:•			em_htg_mam:* em_htg_mam:*	em broo him.	em_htgo_mus:*	1) 1
uclei	Жау	33		94.	of hit	length:					i ii i		9 4	ដដ	<u> </u>	15:	17:	19:	223	8	52.5	52.5		30:	CO C	100	8 6	4 4	
OK nucleic - n	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number o	Minimum DB seq Maximum OB seq	Post-processing:	Database :																					

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	AX418515 Sequence	AX418596 Sequence	AX418534 Sequence	AX418533 Sequence	AX418535 Sequence	AX418521 Sequence AC112761 Rattus no	AC118309 Rattus no	AC094031 Rattus no	AX194850 Sequence	AX467748 Sequence	M74517 Mouse GA Di M74516 Mouse GA bi	BC013558 Mus muscu	ALB44555 Mouse DNA	AF165124 Homo sapi	ACO91926 Homo Bapi	AF320617 Mus muscu	AC109717 Rattus no	AP003001 Mesorbizo	AC100516 Mus muscu	ALCORDING BADI	AC110030 Mus muscu	AC122907 Mus muscu APC03581 Nostoc so	AX432902 Sequence	AR385706 Sequence	AEGOGIOS ANTICODIUM AEGOGIOS RETRODIUM	AC084612 Caenorhab	ACU4186 HOMO BADI	AL121932 Human DNA	295704 Human DNA B	ALISASS Homo sapi	_	HOMO eque:		CANCAMIT OF THE STATE !						OF ILLINOIS (US)
SUMMRIES	AX418515	AX418596	AX418534 BY418532	AX418533	AX418535	AC112761	AC118309	AC094031	AX194850	AX467748	MUSGAC	BC013550	AL844555	AF165124	AC091926	AF320617	AC109717	AP003001	AC100516	AL626782	AC110030	AC122907 AP003581	AX432902	AR385706	AB000102	CBRG44D18	AC140870	H9A373N24	HS4PTEL	AL354817	AL671879	AC140865 A79351	ALIGNMENTS	מעת כל ננ	nt W00200006.	380			biogensor for long	Patent: WO 0250006-A 1 03-JAN-2002; THE BOARD OF TRUSTEES OF THE UNIVERSITY
	.0 33	.0	200	000	7 50	33	8 234801	8 244180	4.75	4 1248	• •	4 2622	4 122211	4 195909	4 209836 8 1254	8 17683	8 226911 8 312050	8 345783	2 61580	2 177264	2 207051	2 233904	6 1018	1122	6 10242	6 42430	6 84743	6 85952	6 118767	6 171310	6 176995	60.6 226349 2 60.6 236165 6			+	15.1 GI:21523	tic construct	cial sequences	and Li, J. c acid enzyme	. WO 0250006-A ARD OF TRUSTRE
Score	33	33 1	27.8	26.4	24	21.8	21.4	21.4	20.6	20.6	20.6	50.6	9.0	20.6	20.6	20.4	20.4	20.4	20.5	7 77	20.2	200	202	500	200	000	2 6	8	50	20 00	25	20 20			ITION Sequence SION AX418515		ORCE Synthetic CORGANISM Synthetic C			JOURNAL Patent THE BO
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Patent: MO 0200006-A 18 03-JAN-2002;
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Location/Qualifiers
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Patent: NO 020006-A 19 03-JAN-2002;
THE BOAR OF TRUSTES OF THE UNIVERSITY OF ILLINOIS (US)
Location/Qualifiers
1. 50
/corganism="synthetic construct"
/mol type="unassigned DNA"
/db fref="taxon:32630"
/db fref="taxon:32630"
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84.2%; Score 27.8; DB 6; Length 50;
Best Local Similarity 93.5%; Pred. No. 0.28;
Matches 29; Conservative 0; Mismatches 2; Indels
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80.0%; Score 26.4; DB 6; Length 50;
Best Local Similarity 96.4%; Pred. No. 1.1;
Matches 27; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 96.4%; Pred. No. 1.1;
Matches 27; Conservative 0; Mismatches 1;

    .50
    /organisme"synthetic construct"
/mol_type="unassigned DNR"
    /db xref="texon:32630"
    /noTe="En-DNR"

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                                                               2 ATCTCTTCTCCGAGCCGGTCGAAATAGTGAG 32
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Sequence 18 from Patent W00200056.
AX418532
AX418532.1 GI:21523397
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Nucleic acid enryme biosensor for ions

Parent: WO 020006-A 82 03-JAN-2002;

THE BOARD OF TRUSTRES OP THE UNIVERSITY OF ILLINOIS [US)

Location/Qualifiers

1. .33

/Organism="synthetic construct"
/mol_type="unassigned DNA"
/Ab_xref="taxon:33630"
/note="Description of Combined DNA/RNA Molecule: Chimeric substrate"
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/mol_type="unassigned DNA".
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Nucleic acid ensyme biosensor for lons
Patent: WO 020006-A 20 03-JAN-2002;
THE BGARD OF TRUSTEES OF THE UNIVERSITY OF
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100.0%; Score 33; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 33; Conservative 0; Mismatches 0
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/mol_type="unassigned DNA"
/db_xref="texon:32630"
/note="Zn-DNA"
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AND
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Sequence 20 from Patent W00200006.
AX418534
Location/Qualifiers
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AX118534
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 Rattus norvegicus
ORGANISM
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JOURNAL
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Rattus norvegicus clone CH230-51A1, *** SRQUENCING IN PROGRESS ***, An unordered pleces.
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Nucleic acid ensyme biosensor for ions
Nucleic acid ensyme biosensor for ions
Patent: WO 020006-A 21 03-JAN-2002;

THE BOARD OF TRUSTERS OF THE UNIVERSITY OF ILLINOIS (US)

Location/Qualiflers
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Nucleic acid enzyme biosensor for jons
Patent: Wo 0200016-A 7 03-JAN-2002;
THE BOAND OF TRUSTEES OF THE UNIVERSITY OF ILLINOIS (US)
Location/Qualifiers
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/db_trype="taxon:25630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.1%; Score 21.8; DB 6; Length 33; 78.8%; Pred. No. 1.18+02; ive 0; Mismatches 7; Indels
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                                linear
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AC112761.5 G1:25006812
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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/organism="synthetic construct"
/wol_type="unassigned DNA"
/db_xref="texon:32630"
/noTes="Zn-DNA"
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                                DNA
                             Sequence 21 from Patent W00200006.
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Sequence 7 from Patent W00200006.
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individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the setimated size. The sequence may sized gaps filled with Ns to the setimated size. The sequence may axer and beyond the ends of the clone and there may be sequence contigs within a contigs scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome tablegun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine
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Rattus norvegicus clone CH230-212018, *** SEQUENCING IN PROGRESS
***, 5 unordered pieces.
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3 22502; gap of unknown length
3 223530; contig of 1028 bp in length
1 227565; contig of 1835 bp in length
Location/Qualifiers
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/db xrsfe="taxon:10116"
/clone="CH230-51A1"

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/note="wgs end extension
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AUTHORS
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Center: Baylor College of Medicine
Center: Cade: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project information
Center project name: GTAA
Center clone name: GT
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.bgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contigs-scaffold, individual sequence contigs are ordered and ordented, and separated by sixed gaps filled with Ns to the estimated size. The sequence contigs are ordered clone and there may be sequence contigs within a contigs-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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NOTE: This is a "working draft' sequence. It currently consists of 5 contigs. The true order of the piaces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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/note="clone_boundary
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225726. .227372
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Rattus.

16 (Bases I to 244180)

18 Marry, D. Marrie., Merker, M. Lee., Abramzon, S., Adams, C., Allen, T., Allen, H., Alsbrooks, S., Amin, A., Augutano, D. Allen, C., Allen, T., Alsbrooks, S., Amin, A., Augutano, D. Allen, C., Allen, T., Alsbrooks, S., Amin, A., Augutano, D. Allen, C., Allen, T., Alsbrooks, S., Amin, A., Baden, H., Baldwin, D., Bundermanke, D., Barber, M., Barnsted, M., Bans, C., Burch, F., Burch, T., Calenco, B., Chen, J., 
Actus norvegicus clone CH230-53XZ0, *** SEQUENCING IN PROGRESS Actus in unordered pieces.
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1 (bases 1 to 244180)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butaleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
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HTG! HTGB PHABL! HTGS DRAFT! HTGS_RNRICHED.
Rattus norvegicus (Norvey rat)
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ley, K.C.
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Olrect Submission

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0; Gaps

64.8%; Score 21.4; DB 2; Length 234801; 80.6%; Pred. No. 3.2e+02; cive 0; Mismatches 6; Indels 0;

Local Similarity 80.6

Best Loca Matches

Query Match

222506 TCTCTTCTCTGAGCCCATCCAATACTTAGT 222536

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RESULT 10

3 TCTCTTCTCCGAGCCGGTCGAATAGTGAGT 33

PLN 14-JUL-1995

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/procein_id="AACij785.1"
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| notes="catalytic submit of a cyclin-dependent kinase component of RNA polymerase II holoenzyme; required for responses to positive and negative regulators; gene also called UNES, GenBank Accession Number L27151"

| product="srblog"
                                                                        SCU20222

Saccharomyces cerevisiae RNA polymerase II holoenzyme
cyclin-dependent kinase component catalytic subunit (SRB10) gens,
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302. .296K
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1 (bases 1 to 3356)
Liao,S.M., Zhang,J., Jeffery,D.A., Koleske,A.J., Thompson,C.M., Chao,D.M., Viljoen,M., van Vuuren,H.J. and Young,R.A.

A kinase-cyclin pair in the RNA polymerase II holoenzyme
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Submitted (24-JAN-1995) Sha-Mei Liso, Whitehead Institute for
Biomedical Research, Nine Cambridge Center, Cambridge, MA C2142,
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/orrain="S288c"
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Saccharomyces cerevisiae
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/genea#SRB10"
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/gene="SRB10"
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/gene="SRB13"
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics. Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON MAY 10, 2003 this sequence version replaced gi:24942156. The sequence in this sequence version replaced gi:24942156. The sequence in this sequence combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.ben.tmc.edu/projects/rat/). Rach coortig described in the feature table below represents a scaffold in the Atlass (http://www.hgsc.ben.tmc.edu/projects/rat/). Rach contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the setimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-belp@bcm.tmc.edu

Contact: hgsc-belp@bcm.tmc.edu

Center project information
Center project name: GRQA
Center clone name: CH230-53K20
Center clone name: CH230-53K20
Center clone name: CH230-53K20
Consensus quality: 209969 bases at least Q40
Consensus quality: 21844 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doce/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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/organisme.Rattus norvegicus"
/mol_type="genomic DNA"
/db_Xref="taxon:10116"
/clone="CH230-53K20"
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/note="wgs_contig"
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113849. .115336
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236001. .237221
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RESULT 12

RESULT 11

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/gene="GABP"

132. 1178

/gene="GABP"

132. 1178

/gene="GABP"

/protein id="GABP"

/protein id="AAA53032.1"

/protein id="GABPITCHARASONDAYNACHARASONDAYNACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHARASONGATETANHACHACHARASONGATETANHACHARASONGATETANHACHACHACHARASONGATETANHACHACHARASONGA
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MUSGAB
MOUSE GA binding protein (GABP-betal subunit) mRNA, complete cds.
M74516 W74512
M74516. I GABP-betal subunit) mRNA, complete cds.
M74516.1 GI:193384
M74516. I GI:193384
M74516. I GI:193384
M18 musculus (house mouse)
M18 musculus (house mouse)
M18 musculus
M2A-binding protein
M2A-binding protein
M2A-binding protein
M2A-binding protein
M2A-binding M2A-bindins
M2A-CO., Byers, B.P., Walton, E.M. and
MCRNight, S.L.
                                                                                                                                                                                                                  MUSGAC hinding protein (GABP-beta2 subunit) mRNA, complete cds. N74517 M74513 M74513 M74513 M74517.1 GI:193412 M74517.1 GI:193412 MV4517.1 GI:193412 MV4517.1 MV477.1 MV477.1
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LaMarco, K., Thompson, C.C., Byers, B.P., Walton, E.M. and
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Identification of Ets- and notch-related subunits in GA binding
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/db_xref="taxon:10090"
/dev_stage=="8.5 day old embryo"
1. 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 253 (5021), 789-792 (1991)
91343912
1876836
168 TCTTCTCCGAGCCGGTGTAAGTAGAGA 194
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                                            PAT 28-AUG-2001
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                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ets-transcription factor related compound specific promoter and
transactivators thereof
transactivators thereof
transactivators thereof
Aganter: WO 0236620-A 12 10-WAY-2002;
Myocontract Pharmaceutical Research AG (CH)
Location(Qualifiers
1.028anism="synthetic construct"
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/db_xref="taxon:32630"
/note="DNA sequence encoding GABFbeta_VP16"
                                                                                                                                                                                                                                                                                                                                                                                                        Chu.T., Blumenfeld, M. and Cohen, D.
Biallelic markers derived from genomic regions carrying genes
livolved in central nervous system disorders
Patent: WO 0151659-A 320 19-JUL-2001;
GENSET (FR)
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/note="downstream amplification primer, complement"
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62.4%; Score 20.6; DB 6; Length 475;
Best Local Similarity 85.2%; Pred. No. 4.5e+02;
Matches 23; Conservative 0; Mismatches 4; Indels
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/note=upstream amplification primer"
312. .351
/note="18-523-352.mis1, potential"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353. .371
/noce="18-523-352.mis2, complement"
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/note="18-523-352 potential probe"
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                                        AX194850 475 bp [ Sequence 320 from Patent WO0151659. AX194850

    475
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 12 from Patent WO0236620.
AX467748
AX467748.1 GI:21900918
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synthetic construct
artificial sequences.
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5 TCTTCTCCGAGCCGGTCGAAATAGTGA 31

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NIW-WGC Project URL: http://mgc.nci.nih.gov
contact: wGC halp dask
Email: cgapba-r@mail.mih.gov
Triseue Procurement: Gilbert Smith, Ph.D.
Triseue Procurement: Gilbert Smith, Ph.D.
CDMA Library Preparation: Life Technologies, Inc.
CDMA Library Preparation: Life Technologies, Inc.
CDMA Library Presquention: Life Technologies, Inc.
CDMA Sequencing by: The I.M.A.G. E. Consottium (LIANL)
Mach Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 11 Row: d Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: marched mRNA gi: 5751933.
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/product=dapph protain"
/product=dapph protain"
/product=dapph protain"
/db_xref="G1:1548885"
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/note="Arp; Region: FOG: Arkyrin repeat [General Eunction prediction only]"
/db_xrefe=CDD:COG0666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-shgc.stanforg.euu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                      Direct Submission

Submitted (04-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor
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/ organism="Mus musculus"

/ organism="Mus musculus"

/ db zref='taxon:10090"

/ db zref='taxon:10090"

/ clone='MGC:6201 IMAGR:3592119"

/ clone='MGC:6201 IMAGR:3592119"

/ clone='MGC:6201 IMAGR:3592119"

/ clone='nype='Mammary tumor metaetatized to lung 'Tumor arose spontaneously from a senescent normal mammary (clona) outgrowth infected with the virus MCTV."

/ clone='lb='NGC CGDP_Lu29"

/ lab_hGst="NH10B"
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         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
23389337
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/gene="Gabpb1"
/db_xref="LocusID:14391"
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Strausberg, R.
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1. (bases 1 co. 2622)

1. (bases 1 co. 2621)

1. Straubberg,R.L., Feingold,R.A., Grouse, L.H., Derge,J.G., Raniata,R.P., Collins,F.S., Magner,L., Schaefer,C.F., Schuler,G.D., Altechul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Hard,P., T., Hang,L., Blacchin,R., Marusina, K., Parner,A.A., Rubin,G.M., Hong,L., Stapleton,M., Sozee,M.B., Bonaldo,M.F., Casavant,T.L., Sozee,M.B., Sozee,M.B., Cayacllano,G.M., Peters,G.J., Maranina,R.Y., Bonaldo,M.F., Casavant,T.L., Sozee,M.B., Bonaldo,M.F., Casavant,T.L., Abramon, R.D., Mullahy,S.J., Bosak,S.A., Conclud., N.A., Peters,G.J., Morenan,R.J., Morenan,P.J., Malek,J.A., Gunaratne,P.H., Richards,G., Willalon,D.K., Marzhy,D.W., Sodergren,B.J., Lul,K., Gibbs,R.A., Voung,A.C., Blutchenko,Y., Walting,M., Madan,A., Young,A.C., Shevchenko,Y., Butterfield,Y.S., Karywinski,M.I., Saalska,U., Saallus,D.B., Dickson,M.C., Rodriguez,A.C., Grimmond,U., Schmutz,J., Myers,R.M., Schnetz,R.A., Schein,J.B., Onose, S.J. and Marza,M.A., Schein,J.B., Schein,J.B., Onose, S.J. and Marza,M.A., Schein,J.B., Sch
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BC013558
BC013558.1 GI:15488854
                                                                                                                                                                                                                Original source text: Mus musculus (strain CD-1) 8.5 day old embryo cDNA to mRNA.
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    Identification of Rts- and notch-related subunits in GA binding
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                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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product="da binding protein"
protein [da"AAAA53031.1"
db_xref="G1:567202"
                                               protein
defence 253 (5021), 789-792 (1991)
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/gene="GABP"
/note="betal subunit"
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Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.

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Consensus quality: 113678 bases at least Q40
Consensus quality: 129742 bases at least Q20
Consensus quality: 13578 bases at least Q20
Consensus quality: 13578 bases at least Q20
Estimated insert size: 140125; sun-of-contigs estimation
Estimated insert size: 140125; sun-of-contigs estimation
Outlity coverage: 4.31 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a working draft's sequence. It currently
* Consists of 21 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* This sequence will be preserved.
* 15399 37410; contig of 1305 bp in length
* 15499 37410; contig of 1305 bp in length
* 44825 54080; contig of 1305 bp in length
* 57421 57522; gap of unknown length
* 57423 57522; gap of unknown length
* 57423 57522; gap of unknown length
* 57424 57522; gap of unknown length
* 57425 5522; gap of unknown length
* 57426 5522; gap of unknown length
* 57427 5752; gap of unknown length
* 57428 5522; gap of unknown length
* 57429 5522; gap of unknown length

necourt 141132 bp DNA linear HTG 23-APR-2001 box sepiens chromosome 5 clone CTB-58H17, WORKING DRAFT SEQUENCE, accossed
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unknown length
                                                                                                                                                                                      ACCO8684.5 G1:9256028
HTG5 FHG8 FHG8_DRAFT; HTG8_ACTIVEFIN.
HTG9 REAGERS (human)
HGG0 SED1688
BULARLYOCKS, Metazoa, Chordaca; Craniata; Verte
BULARLYOCKS, BULHCHIA; Primarces; Cararhini; Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Project Name: 86661, H338
Center clone name: CIT9785KB_59H17
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Sequencing of Human Chromosome 5
Unpublished
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DOB Joint Genome Institute.
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phread quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIS subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at the WORMPEP databases can be found at the NORMPEP database can be found at the NORMPEP datab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-NOV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries:
humqueryeanger. ac.uk Clone requestes: clonerequestesanger.ac.uk
On Nov 19, 2002 this sequence version replaced gi:24939848.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
shotgun may have been used to confirm this sequence.

Beguence data
a phred quality of at least 30.
                                                                                                                       AL844555 122211 bp DNA linear ROD 15-NOV-2002
Mouse DNA sequence from clone RP23-25182 on chromosome 2, complete
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Mus musculus
Bukaryota, Metazos, Chordata, Craniata, Vertebrata, Buteleostomi,
Mummalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 122211)
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For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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Contact: humquery@sanger.ac.uk
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/clone_lib="RPCI-23"
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of 15991 bp in length unknown length of 2947 bp in length unknown length

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Length of 4569 bp in unknown length o£ 4714 of 2703 bp in lunknown length

RESULT 18

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/producte and aninobutyric acid A receptor gamma 2 product gamma-aminobutyric acid A receptor gamma 2 complement (join (70096 ...)0371.74151. ...14356_81148 ...$1300, 119446 ...119583,122155 ...122237,125614 ...125834 ...127937,122493 ...122644,155362 ...155468])
/gamma-Gabbardza* ...129644,155362 ...155468])
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Homo sapiens chromosome 5 clone RP11-290G6, complete sequence.
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DOB Joint Genome Institute.
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 54598, USA 18 Dases 1 to 20986) DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 209836)
2 DOB Joint Genome Institute and Stanford Human Genome Center.
5) Inset Submission
5 Dupublished
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Draft Sequence Produced by DOB Joint Genome Institute
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Submitted (30-AUG-2001) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 2098)6)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Matches 23; Conservative 0; Mismatches 4; Indels 0;
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Pinishing Completed at Stanford Human Genome Center
Parishing Completed at Stanford Human Genome Center
Wev-Sagg. stanford.edu
Quality. Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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:19446. .119383,122155. .122337,125614. .125834,
127910. .127977,129493. .129644,155362. .>155468))
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    (bases 1 to 195909)
    Jiang, S., Yu,J., He,L. and Yang,H.
    Direct Submission
    Submitted (02-JUL-1999) Numan Genome Center, Institute of Genetics, Chinese Academy of Sciences, Datum Road, Beijing 100101, People's

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04106 104007: contig of 1632 bp in length 164108 10517: contig of 1810 bp in length 16518 105297: contig of 1810 bp in length 16518 105297: contig of 1810 bp in length 16618 106298: contig of 1810 bp in length 16929 110028: gap of unknown length 16946: contig of 6317 bp in length 16946: contig of 6317 bp in length 1784: gap of unknown length 1784: gap of unknown length 1784: contig of 3513 bp in length 1785: contig of 3513 bp in length 1785: contig of 3513 bp in length 1785: contig of 4915 bp in length 1787: gap of unknown length 1787: gap of unknown length 1787: gap of unknown length 1787: contig of 4915 bp in length 1787: contig of 4915 bp in length 1887: contig of 4915 bp in length 1887: contig of 1880: pp in length 1887: contig of 1880: pp in length 1881: contig of 1880: pp in length 1880: contig of 1880: pp in length 1880: contig of 1880: pp in length 1880: contig of 1880: contig o
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/clone_lib="CalTech human BAC library B"
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/chromosome="5"
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Sloan-Kettering Cancer Center, 1275 York Ave. RRL 937, New York,
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AC109717
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,

Rummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases I to 17683)

Kalantry, S., Manning, S., Haub, O., Tomihara-Newberger, C., Lee, H.G.,

Pangman, J., Disteche, C. M., Manova, K. and Lacy, B.

The amnionitess gene, essential for mouse gastrulation, encodes a
visceral-endoderm-specific protein with an extracellular
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                                                                                                                                                                                                                                                                                                                  PAT 22-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum
Bharyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sessions, A., Briggs, S., Coopar, B., Goff, S.A., Moughamer, T., Glazebrook, J., Katagiri, P., Kreps, J., Provart, N., Ricke, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                 Cape
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Malatry, E., Haub, O. and Lacy, E.
Direct Submission.
Submitted (13-NOV-2000) Molecular Biology Program, Memorial
                                                                                                   Query Match 62.4%; Score 20.6; DB 9; Length 209836; Best Local Similarity 85.2%; Pred. No. 7.1e+02; Matches 23; Conservative 0; Mismatches 4; Indels 0;
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Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Nismatches 6; Indels 0
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Identification and characterization of plant genes
Identification and characterization of plant genes
Patent: WO 03000904-A 103 03-JAN-2003;
Syngenta Participations AG (CH)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    linear
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Mus musculus strain RIII MRCKbeta gene sequence.
AF320617
                                                                                                                                                                                                                                                                                                                    AX658830 1254 bp DNA Sequence 103 from Parent WO03000904.
AX658830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .1254
/organism="Triticum asstivum"
/mol_type="unassigned DNA"
/db_xref="taxon:4565"
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                                                                                                                                                                                                       180805 TCTCGTCACCGAGCCCGTTGAAATAGT 180831
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Nat. Genet. 27 (4), 412-416 (2001)
                                                                                                                                                                                     3 TCTCTTCCGAGCCGGTCGAATAGT 29
                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (bread wheat)
              /db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-290G6"
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1. (bases 1 to 22691)

B. Allen, C., Allen, H., Alsbrooks, E., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, E., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, E., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, E., Amin, A., Anguiano, D., Allen, C., Allen, H., Adgal, M., Barneted, M., Benahmed, F., Baldwin, D., Bandaranalke, D., Barber, M., Barneted, M., Brown, M., Baldwin, D., Bandaranalke, D., Barber, M., Byth, P., Brown, M., Baldwin, D., Bandaranalke, D., Barber, M., Byth, P., Chor, E., Cardenas, V., Cherck, J., Chaver, D., Charder, C., Cardenas, V., Cherck, J., Charler, C., Cardenas, C., Chen, B., Chas, C., Charler, C., Cardenas, C., Chen, G., Coyle, M., Cree, A., D'Soura, L., Davila, M.L., Davis, C., Davila, Y., Chen, C., Coreland, C., Davila, M., Cree, A., D'Soura, L., Dayla, M., Darsen, G., Durn, A., Durbin, K., Duval, B., Eaves, M., Pengado, D., Denson, S., Dersen, C., Evans, C.A., Falls, T., Fan, G., Fager, P., Fraser, C.M., Gabisi, A., Gare, R., Garer, T., Garze, M., Gebragoryis, B., Geer, K., Gill, R., Garcia, A., Garera, M., Gebragoryis, B., Hall, M., Hamil, C., Hamilton, C., Hamilton, K., Harley, Y., Halles, S., Hadun, S.L., Hodgson, A., Hogue, M., Hamil, S.L., Hodgson, A., Hogue, M., Hans, S., Harley, J., Gora, C., Lewis, L., Liu, J., Jacob, L., Laboy, H., Levas, J., Lewis, L., Liu, Y., London, P., Longacre, S., Lorgez, J., Liu, W., Liu, Y., London, P., Longacre, S., Lorgez, J., Liu, W., Liu, Y., London, P., Longacre, S., Lorgez, J., Lorgenniew, M., Mahmald, M., Mahmald
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226911 bp DNA linear HTG 11-OCT-2002
Rattus norvegicus clome CH230-302F7, WORKING DRAFT SEQUENCE, 2
ACIOCATA
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Location/Qualifiers

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4. Ab Arrel = "taxon:10090"

/ Ab Arre
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Rattus norvegicus (Norway rat.)
Rattus norvegicus
Rattus norvegicus
Battus norvegicus
Bukaryota; Metaroa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%; Score 20.4; DB 10; Length 17683;
80.0%; Pred. No. 7.2e+02;
1ve 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16564 TCTTTTCTCCGAGAGGCCAGAAGAGTCAG 16535
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Best Local Similarity 80.00
Matches 24, Conservative
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Mycobacterium leprae otrain TM complete genome; segment 3/10.
AL581319 AL450180
AL581319.1 GI:13092766
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Submitted (20-PBB-2001) Submitted on behalf of the Mycobacterium
leprae sequencing teams, The Sanger Centre, Wellcome Trust Genoma
Campus, Minxton, Cambridge, CB10 18A, UX Unitie de Genetique
Moleculaire Bacterianne, Innstitut Pasteur, 28 rue du Docteur Rouux,
75724, Paris Cedex, Prance, E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Dassel to 31200)
1 (Danier, P. Rathill, J., James, K.D., Thomson, N.R., Mhogall, K., Basham, D., Brown, D., Chillingworth, T., Connor. R., Hangall, K., Basham, D., Brown, D., Chillingworth, T., Connor. R., Hamlin, N., Holroy, S., Hornsby, T., Jagels, K., Lacroix, C., Maclean, J., Moule, S., Murphy, L., Oliver, Quall, M.A., Simon, S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Details of M. leprae sequencing at the Sanger Centre are available
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Location/Qualifiers
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Mycobacterium leprae
Bacteria, Actinobacteria; Actinobacteridae, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Best Local Similarity 80.0%; Pred. No. 8.88+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0;
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                                                                           1. .226911
/ organism="Rattus norvegicus"
/ mol. type="genomic DNA"
/ db xref="taxon:10116"
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1. .1189
/ note="wag end extension
clone=maispe"
1240. .2418
/ note="wag end extension
clone=maispe"
/ note="wag end extension
clone end:5pe"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end sequence: RXAKG28TV*
217999. .18035
/note="clone_boundary
clone_end: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end_sequence : EXAKG28TJ"
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Puzzo, K., Poindexter, A., Popovic, D., Primus, K., Pu. L.-I.,
Puzzo, W., Guiroz, J., Rachlin, B., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S.,
Rigges, P.,
Rives, C., Rodkey, T., Ren, Y., Reuter, M., Robe, R., Ruiz, S.J.,
Sandors, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Sneed, A., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Sneed, A., Savery, B., Suga, X.-Z., Sorelle, R., Sosa, J.,
Steimle, H., Strong, R., Sutton, A., Evatek, A., Tabor, P.,
Taylor, T., Thomas, M., Thomas, R., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasan, D., Waldron, L., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,
Willson, G., Willson, R., Wilson, R., Wilson, Worley, V.,
Wright, D., Wright, R., Wu, J., Zhou, K., Zhoo, S., Dunn, D., Yon, P.,
Weinstock, G. and Gibbs, R. A.
Direct Submission

A. Unpublished

The Company of the Company o
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On Oct 11, 2002 this sequence version replaced gi:21738139.

The sequence in this assembly is a combination of BAC based reads and whole genome shockun sequencing reads assembled using Atlas and whole genome shockun men-edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a contig easificated, Within each contig easificated, and separated by sized gaps filled with Ns to the estimated airs. The sequence only give a contig within a contig of the clone and there may be sequence contigs within a contig seaffold that consist entiraly of whole genome shockun sequence reads. Both and sequences and whole genome shockun sequence reads. Both end sequences and whole genome table.
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center clone name: GQIX
Center clone name: GAI30-302P7
Center clone name: GAI30-302P7
Center clone name: GAI30-302P7
Consensus quality: 215491 hasse at lesst Q40
Consensus quality: 215491 hasse at lesst Q30
Consensus quality: 215491 hasse at lesst Q30
Consensus quality: 2154975 hasse at lesst Q30
Consensus quality: 2154975 hasse at lesst Q30
Consensus quality: 216975 hasse at lesst Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-PEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicins, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 226911)
Rat Genome Sequencing Consortium.
Direct Submission
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17 225796: gap of unknown length
17 226911: contig of 1115 bp in length.
Location/Qualiflers
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Center code: BCM
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Direct Submission
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PEATURES

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REPERENCE AUTHORS TITLE JOURNAL

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes Similar to M. tuberculosis pgk, Rv1437, phosphoglycerate kinase, SW:PGK_MVCTU (006821) (412 aa); Pacta scree E(): 0, 0. 0. tidently in 412 aa overlap. Similar to many w.g. Corynebacterium glucamicum pgk, phosphoglycerate kinase, SW:PGK_COGG, (001655) (4613 aa); Pacta score E(): 0, 59.24 identity in 407 aa overlap. Previously sequenced as SW:PGK_COGG, (001655) (416 aa); Pacta score E(): 0, 99.84 identity in 407 aa overlap. Contains Pfem match to entry PP00162 PGK, Phosphoglycerate kinases. Contains PS00111 Phosphoglycerate kinase
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active site"
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1962. .7994
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Mescrhizobium loti DNA, complete genome, section 8/21.
AP003001 BA000012 .
AP003001.2 GI:14023393
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DNA Res. 7 (6), 331-338 (2000)
                                                                                                                                                                               Direct Submission

Direct Submission

Submitted (05-DEC-2000) Takakaru Kaneko, Karusa DNA Research
Submitted (16-DEC-2000) Takakaru Kaneko, Karusa DNA Research; Yana
1532-3, Kisararu, Chiba 292-0812, Japan
1532-3, Kisararu, Chiba 292-0812, Japan
(RE.mail:Ranekodkarus or:Jp
(RE.mil:Ranekodkarus or:Jp)

Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)

Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)

Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)

Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
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Mesorhizobium loti
Mesorhizobium loti
Bacteria, Prochacteria, Alphaprotechacteria, Rhizobiales,
Phyllobacteriaceae; Mesorhizobium.
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61.8%; Score 20.4; DB 1; Length 312050;
Best Local Similarity 80.0%; Pred. No. 9e+02;
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SITTON, B., INITON, L., NUSDAUN, C., LANDGE, E., All, A., Allen, N., Allen, N., Anderson, S., Barran, N., Bastian, V., Boguslavkiy, L., Boukbgalter, B., Anderson, S., Camarata, J., Camarata, J., Camarata, J., Camapoplano, A., Collymore, A., Cook, A., Chararo, E., Choppel, Y., Colangopiano, A., Collymore, A., Cook, A., Cook, P., Colangopiano, A., Calymore, A., Cook, A., Cook, P., Diaz, J.S., Dodge, S., Paro, S., Perreira, P., Pitzhugh, M., Goyette, M., Garan, J., Garagna, S., Gord, S., Goyette, M., Garan, L., Garador, P., Farreira, P., Farreira, P., Farreira, M., Garata, M., Maratas, M., Marather, C., Lagocque, K., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lagocque, K., Liu, G., Lamazare, R., Landera, F., Landera, T., Marguis, N., Matthews, C., Macdanald, P., Major, J., Marguis, N., Matthews, C., Macdanald, P., Major, J., Marguis, N., Matthews, C., Macdanald, P., Major, J., Marguis, N., Matthews, C., Norman, C., McGanald, P., Major, J., Marguis, N., Maley, R., Ras, C., Raditim, J., Robert, M., Piare, R., Pollara, V., Nathura, C., Retta, R., Palanga, V., Plarre, M., Pollara, V., Nathura, C., Retta, R., Robert, M., Riley, R., Rise, C., Rogov, P., Strauss, N., Subremanian, M., Talanas, J., Tesfaye, S., Theodore, J., Tophan, K., Willson, B., Wu, X., Wyman, D., Ve, W.J., Voung, G., Zainoun, J., Zabek, L., Zimmer, A. and Zody, M.

Research, J20 Charles Street, Cambridge, MA 02141, J3A
All repeate were identified using Repeathasker:

Center: Whitchead Institute/ MIT Center for Genome Research
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Mus musculus clone RP23-145H2, LOW-PASS SEQUENCE SANPLING.
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Birren,B., Linton,L., Nushaum,C. and Lander,E.
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Mus musculus
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9912. .10376
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26541: contig 26541: contig 27331: cont of 27431: gap of 28129: contig 28982: contig		30714: gap or 100 bp 31454: contig of 740 bp in 31554: gap of 100 bp	32365: COBC19 32365: Gap of	33168: gap of 100 bp 33875: contid of 707 bp in	33975: gap of 100 bp 34691: contig of 716 bp in	34791: gap of 100 bp 35515: contig of 724 bp in	35615: gap of 36311: contig of	36411: gap of 10 37119: contig of	37889: contig of 1	38725: contig o	39512: contig of 687 39612: gap of 100 bp	40440: gap of 1	41267: gap of 100 bp 41996: contig of 729 bp in	42096: gap of 100 bp 42807: contig of 711 bp in	42907: gap of 43628: contig	44438:	45280: contig	46132; contig	46936: contig	47036: gap of 47750: contig	47850: gap of 48574: contig	48674: gap of 100 bp 49408: contig of 734 bp in 1	49508: gap of 100 bp 50220: contid of 712 bp in	50320; gap of 15¢ bp 51038; contid of 718 bp in 1	51138: gap of 100 bp	51956: gap of 100 bp	52658: contig 52758: gap of	53469: contig		55108: contig
25838 26542 26642 27332 27432 28130 28130	29983 29793 29893	30715	32266	33069	33876	34792	35516	36412	37220	37990	38826	39613	41168	41997	42808	43629	44539	45381	46233	46937	47751	48575	49409	50221	51039	51857	51957	52759	53570	54380
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DEFINITION RESULT 27 AC068718/c

Matches

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ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT

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/map="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURES
                                                                                                                                                                                                                                                       161955 bp DNA linear PRI 09-JAN-2002 Homo sapiens BAC clone RP11-123G24 from 2, complete sequence. AC068718 AC068718.6 GI:14718377 HTG.
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Submitted (09-JAN-2002) Department of Genetics, Washington
Submitted (09-JAN-2002) Department of Genetics, Washington
Oniversity, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 14, 2001 this sequence version replaced gi:14573737.
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Submitted (07-KAY-2000) Genome Sequencing Center, Washington
Midversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
WO 63108, USA
4 (bases 1 to 161955)
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Direct Submission

Universalty Rehould Genome Sequencing Center, Washington
Universalty School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 51109, USA

S (bases I to 161955)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeates; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 16195).
Sulston, J. B. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this close. It may be shorter because we only sequence overlapping close sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                             Gaps
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                                            Length 61580;
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Du,P., Moyer,R., Doebber,A. and Dignan,G.
The sequence of Homo sapiens BAC clone RP11-123G24
Ungublished (20D1)
3 (bases 1 to 161955)
Waterston, R.H.
                                                                                             Indels
                                            Score 20.2; DB 2;
Pred. No. 9.7e+02;
0; Mismarches 8;
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Genome Res 8 (11), 1097-1108 (1998)
                                                                                                                                         1 CATCTCTTCTCCGAGCCGGTCGAATAGTGAGT 33
56017: gap of 100 bp
                                                 61.24;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                             25; Conservative
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                                                                      Similarity
                                              Query Match
Best Local S
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SOURCE INPORMATION:

He RPCI-11 human BAC library was made from the blood of one male donor, as described by Ossegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Cartenes, J.G. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics Silles. The Cione may be obtained either from and coworkers at the Roswell Park Cancer Institute

Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute

WECTUR: pbaces.med.buffalo.edul
WECTUR: pbaces.
                     Louis
                                                                                                                                                                                                                                                                                                       Actual start of this clone is at base position 1 of RP11-:23G24; actual end is at base position 161955 of RP11-123G24. Location/Qualifiers
Mapping information for this clons was provided by Dr. John D. McPherson, Department of Genetics, Mashington University, St. 18 MO. For additional information about the map position of this sequence, see http://genome.wistl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                              1. .161955
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1018 . 1077

/ rpt family = AT rich ||

1183 . 1489

/ rpt family = Alu ||
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/rpt_family="(TAAA) n"
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10471, 10772
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10773, 10818
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1768. .11815
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MAPPING INPORMATION restriction digest.

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Direct Submission

Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Kinxton, Submitted (29-JUN-2002)

Cambridgeshire, CB10 15A, UK. B-mail enquiries:
humquerydsanger.ac.uk Clone requeste clonerequestessanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:19011874.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation amnotation may not be found in the sequence subrission
corresponding to the overlapping clone, as we submit sequences with
only as small overlap as described above.

This sequence was finished as followe unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., pixed quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mill subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Bm: EMBL; Sw:
SWISSPROT; Ir:, TREMBL; Wp:, WORWEP; Information on the WORWEP;
database can be found at
                                                                                                            ALG26782 177264 bp DNA linear ROD 29-JUN-2002
Mouse DNA sequence from clone RP23-335N15 on chromosome X, complete
sequence.
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                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (beses 1 to 177264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-335Nl5 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

VBCTOR: pBACe3.6
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Center: OWG: UK-MR
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseg@har.mrc.ac.uk
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                                                                                                                                                                                                                                                                                                                 .4610 . 14862
|notes"similar to Homo sapiens BST AA193339 (NID:gl782929)
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                                                                                                                                                                                                                                                                                                                                                                             4613. .14844
Inotes="similar to BST BI185210 (NID:g14659619)"
4952. .15347
49572. .17368
                                                                       12022 . 13945
/rpt family="SvA"
13927 . 13946
/rpt family="(GAAA)n"
13927 . 13947
/rpt family="(GGAGA)n"
13966 . 14618
/rpt family="11"
14609 . 14953
/note="saimila" to Homo sapiens BST AW977707
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7 rpt family="AT rich"

21689 .21919

7 rpt family="L1"

7 rpt family="CA,n"

22900 .22938

7 rpt family="(CA,n"

22907 .22938
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25473. 25502.
25473. 25502.
25932. 25503.
/rpt_family="Ar_rich"
7505 family="Ar_rich"
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27661. 27822
28513. 28721
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/rpt_family="BRVL"
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29811. 29905

/rpt_family="AT_rich="30015. 30084"

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/rpt_family="MIR"

30352. 30677

/rpt_family="MIR"

30578. 31555
                                                                family=" (T)n"
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1 (bases 1 to 207051)
Birren, B., Linton, L., Nusbaum, C. and Lander, B., Musmuscullus, Clone RP23-49818
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musculus clone RP23-49818, WORKING DRAFT SEQUENCE, 72 ordered
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                                                                                                                                                            HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP. Mus musculus (house mouse)
                                                                                                                           AC110030.3 GI:20455635
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onsists of 72 contigs. Gaps between the contigs are represented as runs of N The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced the finished sequence as soon as it is available and the accession number will be preserved.

Segister of the gap of 100 bp to 100 bp 
                                                             Center project name: L22336
Center clode name: 49 % 8 18
Assembly program: Phrap; version 0.960731
Centernais quality: 186564 bases at least 040
Centernais quality: 186010 bases at least 030
Centernais quality: 198001 bases at least 020
Insert size: 180000; agarose-fp
Insert size: 189951; amm-of-centigs
Quality coverage: 8.1 in Q20 bases; sum-of-certigs
Contact: sequence submissions@genome.wi.mit.edu
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of 948 bp in length
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AP003581 348050 bp DNA linear BCT 28-NOV-2001 Mostco sp. PCC 7120 DNA, complete genome, section 1/19. AP003581 BA000019 AP003581. I GI:17134979
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Ammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
(bases 1 to 233904)
filson, R.K.
                                                             Allean, N.K.
Milean, N.K.
Direct Bubmission
Birect Submission
Bubmitted (30-007-2003) Genome Sequencing Center, 4444 Forest Park
Barkway, E. Louis, NO 63108, USA
4 [basss 1 to 233904)
                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (10-1002) Genome Sequencing Center, 4444 Forest Park
Submitted (10-1001s, WG 51108, USA
On Dec 10, 2003 this sequence version replaced gi:38044277.
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DNA Nes. 8 (5), 205-213 (2001)
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Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
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Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
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Web site:http://www.
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161015 CATCTATATCTGAGCGTCGATAAAGGGGGGTGAGT
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/db_xref="taxor:10090"
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/clone="RP23-4914"
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Kaneko, T.
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kgr"
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complement(901...1718)
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                     Institute, The First Laboratory for Plant Gene Research, Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (B-mail:knnekookazusa.or.jp, URL:http://www.kazusa.or.jp/cyanobase/, Tel:81-438-52-3936 (ex.2338), Pax:81-438-52-3934)
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Unknown.
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Breton, G.L. and Osborne, M.
Nucleic acid amino acid sequences relating to Klebsiella pneumoniae
for diagnostics and therapeutics
Fatent: US 6610836.A 2452 26-AUG-2003;
Patent: US 6610036.A 2452 26-AUG-2003;
Location/Qualifiers
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Rhizobium sp. NGR234 plasmid pNGR234a, section 42 of 46 of the complete plasmid sequence.
AR000105 UD0090
AR000105.1 GI:2182706
                             PAT 18-DEC-2003
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Direct Submission
Submission
Submitted (32-NGV-1996) Genome Analysis, Institute for Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
1 (bases 1 to 10140)
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Direct Submission
Submirted (12-DBC-1997) Genome Analysis, Institute for Molecular
Submirted (12-DBC-1997) Bentenbergstrasse 11, Jena 07745, Germany
Update by submitter
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Rhizobium sp. NGR234
Rhizobium sp. NGR234
Bacceria; Protechacteria; Alphaprotechacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobecterium group; Rhizobium.
L (bases 1 to 10140)
Prehberg, C., Fellay, R., Bairoch, A., Broughton, W.J., Rosenthal, A. and Perret, X.
And Perret, X.
Molecular basis of symbicsis between Rhizobium and legumes
Nature 387 (6611), 394-401 (1997)
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716. .>10140
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                             AR385706 1122 bp DNA Sequence 2435 from patent US 6610836. AR385706.1 GI:40095440
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     AR385706/c
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AUTHORS
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IVLASVAASSNYRIPSGIGNLLEYALEFIRDLANOOIGEEDTRFWYPFYGTLEITY
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VGFWGALVPFKLIHUFFYCLSEAFERHIADELVYGYLVLIVPLFVPLEVRGHGYFCHY
VGFWGALIFATIADAYIGEAFERHIADELVYGYLVLIVPLFVPLEVRGHGYFCHY
COMPIEMENT (9132. .9500)
/Genewarpiement (9132. .9500)
/Genewarpiement (132. .9500)
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GVYYLNHAKDVRELGREKQSLSKTRLALLMALILLASKNNOLOIMPIFLGFLTYKAT
LIIYVVRVRYRFISDSPKLROP"
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Bacillus licheniformis
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Best Local Similarity 82.1%; Pred. No. 8.6e+02;
Matches 23; Conservative 0; Mismatches 5; Indels
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Methods for monitoring multiple gene expression
Patent: WO 0229113-A 1317 11-APR-2002,
Novosymes Biotech, Inc. (US); Novosymes A/8 (DK)
Location/Qualifiers

    1018
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product="ATP synthase subunit a"
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Sequence 1317 from Patent W00229113.
AX432902
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IATBEDGUNGPAPPTGGGARISAYTTGESBIIENTOTITG
DALLYTHSHGROMARELGIPLARIGPPIPDRLGSGOHKLITULYNGTROLIFEAANIIGAN
                OSECPIGLIGDDI BAVSRKKAABHBITI VPVRCEGFRGVSGSLGHLIANDAI RDYVED
KADCKTOVEFBTGPY DVNV IGDYNI GGDANASRILLBEI GLRVVGNNSGDATLAEVER
APBAKINI HCYRSMNI CRHNBRYA, PNGR YNPGPSGI BASIAKI ARHFGFTI BE
BARBVI AKYR PLVDAVI TYMPELGOKRVAL YVGGLRPRHVI TAYEDLGHQI VGTGYE
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AE000102 U00090 AE000102.1 GI:2182680
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alternative start point at nucleotide 492755"
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Direct Submission
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Biotechnology, Beutenbergetrasse 11, Jona 07745, Germany
Update by submitter
Location/Qualifiers
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Direct Submission
Submitted (22-NOV-1996) Genome Analysis, Institute for Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
3 (bases 1 to 10242)
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Prelberg.C., Fellay,R., Bairoch,A., Broughton,W.J., Rosenthal,A. and Perret,X.
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Rhizobium ap. NGR218
Bacteria, Procedacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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60.6%; Score 20; DB 1; Length 10140;

8est Local Similarity 82.1%; Pred. No. 16+03;

Matches 23; Conservative 0; Mismatches 5; Indels
function="nodulation protein"
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CBRG44D18 42430 bp DNA linear INV 04-NOV-2000 Caenorhabditis briggsae cosmid G44D18, complete sequence.
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HOMO Sapiens clone RP11-702C13, LOW-PASS SEQUENCE SAMPLING
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 53371)
Birran, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens, clone RP11-702C13
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Department of Genetics, Washington University,
St. Louis, MO 63110, USA
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Mashington University Genome Sequencing Center.
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1. 42430
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3 (bases 1 to 42430)
Waterston, R.
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                    2986 CTCTTCACCGAGCCGGTCGACCTGCTGA 3013
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HOMO SADIEDS
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Caenorhabditis briggsae
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9334. 8651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical 14.8 kd protein; similar to N-terminus of nitrogenase Fe protein NifH"
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                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical 17.7 kd protein, similar to proteins of other nitrogen-fixing bacteria and to YaxD" /codon start=1 /transL_table=11
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[Avidence:not_experimental
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10752 11497; contig of 746 bp in length 11598 12566; gap of 100 bp 12598 12566; gap of 100 bp 1257 12466; gap of 100 bp 12567 12466; gap of 100 bp 12567 12456; contig of 739 bp in length 1356 14025; contig of 739 bp in length 14026 14025; contig of 739 bp in length 14026 14046; gap of 100 bp 14026 14046; gap of 100 bp 14026 14046; gap of 100 bp 15797 15521; contig of 735 bp in length 15797 15521; contig of 725 bp in length 15797 16521; contig of 725 bp in length 1652 17359; contig of 725 bp in length 17460 18499; gap of 100 bp 17460 18499; gap of 100 bp 18394 18291; gap of 100 bp 18394 18291; gap of 100 bp 18394 18291; gap of 100 bp 18399 19088; contig of 595 bp in length 18899 19088; gap of 100 bp 19899 19088; gap of 100 bp	2164: Gurigi 21554: Gurigi 22257: Gunigi 22257: Gunigi 22357: Gunigi 23925: Gunigi 24042: Countigi 24042: Countigi 24042: Countigi 24042: Gunigi 2558: Gunigi 2558: Countigi 2558: Countigi 2558: Gunigi 26487: Gup of 27713: Gunigi 28147: Gup of 28147: Gunigi 281627: Countigi 281627: Gunigi 281627: Gunigi 281627: Gunigi 281627: Gunigi 281627: Gunigi 281627: Gunigi 281627: Gunigi 281627: Gunigi 31614: Gunigi	33053: 920 of 100 bp 33875: contig of 52 bp in 1 34566: contig of 691 bp in 1 34666: gap of 100 bp 35382: contig of 716 bp in 1 35482: gap of 100 bp 36175: contig of 593 bp in 1 36175: contig of 717 bp in 1 36892: contig of 717 bp in 1 36892: gap of 100 bp 37715: contig of 723 bp in 1 37815: gap of 100 bp 37815: gap of 100 bp 38640: contig of 725 bp in 1 38640: contig of 743 bp in 1 3843: gap of 100 bp 40207: contig of 743 bp in 1 3843: gap of 100 bp 40207: contig of 743 bp in 1 3843: gap of 100 bp 40207: contig of 724 bp in 1 41038: contig of 724 bp in 1
Birren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Anderson, S., Baraia, N., Bastien, V., Beda, F., Boqualavki, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Diaz, J., Garden, S., Gorde, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Glinde, S., Goyette, M., Fitzhugh, W., Gage, D., Galagan, J., Sargias, J., Horton, L., Ilev, I., Johneson, R., Janeson, R., Harquis, R., Landers, T., Lehoczky, J., Levins, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McSwan, P., McKernan, K., Morwe, J., Mirgh, T., Naylor, T., Mihova, T., Mlenga, V., Norman, D., Saldra, J., Minora, T., Connor, T., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Risp, R., Stanger, P., Stanger, Thoman, N., Stojanovic, N., Streamnian, A., Talamas, J., Teleyse, S., Theodore, J., Tirell, A., Travers, M., Trigilio, J., Vassiliav, H., Viel, R., Vo, A., Samco, M., Wilson, B., Wu, X., Wyman, D., Ye, Wassiliav, H., Viel, R., Vo, A., Almser, A., and Zody, M., Trigilio, T., Young, G., Zainoun, J., Zamner, A., and Zody, M., Telwer, A., Sonko, M., Tolamas, J., Young, G., Zainoun, J., Zamner, A., and Zody, M., Telwer, M., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Trigilio, T., Young, G., Zainoun, J., Stoganor, S., Sanger, M., Sander, M., Stoganor, S., Sanger, M., Stoganor, S., Sanger, M., Stoganor, S., Sanger, M., Stoganor, S., S	All repeats were identified using Repeathasker: Sult, A.P.A. & Creen, P. (1996-1997) http://ftp.genome.washington.edu/RM/Repeathasker.html conter: Whitehead institute/ WIT Center for Genome Research Center: Ode: WIBR Web site: http://www-seq.wi.mit.edu Conterc: sequence submissions@genome.wi.mit.edu Conterc: forcom contains 65 individual WOTE: This record contains 65 individual Sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows voverlags reads that may be gene-rich and allowe will be sequenced to completion. In the event that the record is updated, the accession number will be preserved. 724 823 gap of 100 bp 1566 1665: gap of 100 bp 1666 2414: contig of 742 bp in length 1666 2414: gap of 100 bp 1666 2414: gap of 100 bp	2515 3251: Contig of 737 bp in length 3522 4069: contig of 737 bp in length 4070 4169: gap of 100 bp 4070 4169: gap of 100 bp 4070 4663: contig of 694 bp in length 4864 9663: contig of 694 bp in length 4864 9669: contig of 706 bp in length 5670 5769: gap of 100 bp 5770 6498: contig of 726 bp in length 5670 5769: gap of 100 bp 5770 6498: contig of 729 bp in length 7325 7334: contig of 728 bp in length 7325 7334: contig of 728 bp in length 7325 7334: contig of 728 bp in length 8153 8973: contig of 728 bp in length 8153 8973: contig of 728 bp in length 8153 8973: contig of 728 bp in length 8154 9073: gap of 100 bp 8253 8973: contig of 728 bp in length 8154 9073: gap of 100 bp 8155 contig of 728 bp in length 9175: gap of 100 bp 9175: gap of 100 bp 9175: gap of 100 bp 10652 10751: gap of 100 bp
AUTHORS AUTHORS	СОФРЕНИ	

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Concensus quality: 82347 bases at least Q40
Concensus quality: 82345 bases at least Q20
Concensus quality: 82326 bases at least Q20
Concensus quality: 83281 bases at least Q20
Estimated insert size: 175000, agarose-fp estimation
Estimated insert size: 84343, sum-of-contiggs estimation
Estimated insert size: 84343, sum-of-contiggs estimation
Quality coverage: 6.35 in Q20 bases) sum-of-contiggs estimation.

* NOTS: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
it in so Known and their order of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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AL121932.19 GI:8894624
HTG; CpG island.
Homo sapiens (human)
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Direct Submission
Submitted (30-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 13A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone
requests: Clonerequest@sanger.ac.uk
Om Jul 1, 2000 Libs sequence version replaced gi:8346909.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 85952)
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1839: gap of unknown.length
1834: contig of 1395 bp in length
1334: gap of unknown length
1898: contig of Easts bp in length
12880: contig of East bp in length
12880: contig of East bp in length
12880: gap of unknown length
12880: gap of unknown length
184743: contig of 71763 bp in length
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Best Local Similarity 82.1%; Pred. No. 1.2e+03;
Matches 23; Conservative 0; Mismatches 5; Indels
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/clone="RP11-1132B16"
/clone_lib="RPCI bumman BAC library 11"
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                           Project Information
Center Project Name: 1729232
Center clone name: RPCI-11_1132B16
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/organisma"Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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HSA373N24
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AC140870
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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1 (Dases 1 to 8474)

DOB Joint Genome Institute.
Sequencing of Human Chromosome 5

Unpublished

2 (Dases 1 to 8474)

DOB Joint Genome Institute.

Doble denome Institute.
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of 725 bp in length
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HTG; HTGS PHASB1; HTGS_DRAFT; HTGS_ACTIVEPIN.
HOMO sapiens (human)
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/mol_type="genomic DNA"

/db xref="taxon:9606"

/olone=RPD1-702C13"

/clone_lib="RPCI-11 Human Male BAC"
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                  conteponding to the overlapping times, as we seemed a section only a small overlapping as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

BMI. SMRB. SWISSPROT; Tr., TREMBL, Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence was generated from part of bacterial clone contiggs of human chromosome 6, constructed by the Sanger centre Chromosome 6 Mapping Group. Purther information can be found at HTDPLYNY: This sequence is not the entire insert of clone IMPORTANT; This sequence is not the entire insert of clone RPI1-373NX; It may be shorter because we sequence overlapping sections only once, except for a 100 base (overlapping the true right end of clone RPI1-373NX; is at 85592 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were such a pasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest.

RPII-373NA4 is from the library RPII-11.2 constructed by the group of Pieter de Jong. RPI when the table details see
  corresponding to the overlapping clone, as we submit sequences with
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tem"LINCS repeat: matches 7283. .7469 of consensus"
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omplement (4977. .5480)
note="match: GSS: Em:AQ521901"
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/mol_type="genomic DNA"
/db_xrefs"taxon:9606"
/chromosome="6"
/clone="RP1-373N24"
/clone_llb="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.cm.vRCTOR: pBACe3.6.
VRCTOR: pBACe3.6.
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repeat: matches 5169. .5620 of consensus* note="LIMM10 repeat: matches 5596. .6320 of consensus" 2636. .32935 4295, .14509 note="LTR16A repeat: matches 211, .416 of consensus" note="WITCH repeat: matches 474, .504 of consensus" 3254, .33696 ="MER21B repeat: matches 486. .794 of consensus" repeat: matches 15. .6146 of consensus" /note="MITICE repeat: matches 10. .461 of consensus" 4787. .14994 note="LTR16A repeat: matches 1. .211 of consensus" note="PABL A repeat: matches 1. .660 of consensus" /note="AluJo repeat: matches 7. .304 of consensus" 13019. .13372 /note="match: GSS: Em:AQ214591" 13019. .1335 /note="match: GSS: Em:AQ214568" complement(13137. .13417) repeat: matches 2. .310 of consensus" repeat: matches 1. .287 of consensus* repeat: matches 1. .300 of consensus" 9821. .10104 //notes=#Alu8x repeat: matches 3. .299 of consensus" complement (10582. .11236) //notes="match: GSS: Em:AQ586503" 10645. .11098 8944. 9245 /note="AluSx repeat: matches 7. 308 of consensus" repeat: matches 1. .310 of consensus $^{\mu}$ consensus .310 of consensus" repeat: matches 1. .447 of consensus" mote="Alux repeat: matches 5. .311 of consensus" complement(13137. .13417)
/notes*match: GS9: Bm:AQ236371*
/liotes*match: GS9: Bm:AQ288379*
/notes*match: GS9: Bm:AZ36916*
/notes*match: GS9: Bm:AQ9914771* note="natch: STS: Bm:G31524" 13748. .13613)) repeat: matches 1. .236 of 441. .8749 note="Alu8q repeat: matches 2. /note="match: GSS: Em:AZ831171" complement(7839..8442) complement (7839. .8442) //note==match: 0.58: En.A5312892" complement (8160. .8444) /note==match: 088: En.AQ110263" complement (12990, .13351) /note="match: G9S: Ex:AQ382623" complement (12991, .13363) note="match: GSS: Em:AQ747522" 3016. ..13350 note="match: GSS: Em:AQ532682" 3016. .13306 .3306. .13423) 1: GSS: Em:AZ416410" evidence-not experimental 1046, 11384 note-"LTR35 repeat: matche complement (join (13317 note-"CpG island" complement (13306, 14294 note="Alu6x ote-"AluJb note="AluSx note="AluSp

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08. .352
notew*MSREP271 repeat: matches 36. .182 of consensus"
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12005. .12155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ibte="Linc2 repeat: matches 509. .693 of consensus"
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| oct=="il repeat: matches 4800, .5390 of consensus"
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hote="LIPA2 repeat: matches 1. .891 of consensus"
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notes"AluJD repeat: matches 1. .290 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5. .143
note="2 copies of 29 mer 100 % conserved"
                                                                                                                                                                                                                         . .198
mote="11 copies of 18 mer 81 % conserved"
                                                                                                                                                                                                                                                                                                                                                    copies of 61 mer 89 % conserved*
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1452
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                                                   /organisma"Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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note="4 cc
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Human DNA sequence from 4PTEL, Huntington's Disease Region,
chromosome 4p16.3.
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FPTEL is contained in a clone contig spanning

HD which is described in Baxendale et al, Nature Genetics 4 ( 1993 181-186. See also Myers et al, Cytogenet Cell Genet. 66 ( 1994
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                                                                                                                                                                                                                                                                                                                                                    note = "tRNA-Ala-GCG repeat: matches 3. .72 of consensus"
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ammalia; Buthbria; Primates; Catarrhini; Rominidae; Homo.
(bases 1 to 11875)
                                                                                                                                                                                                                                                                                                                                                                                   568. . 18638
CHE*TRNA-Ala-GCG repeat: matches 3. .73 of consensus<sup>*</sup>
850. . 28957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the entire insert of clone 4FTEL. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                      .2 repeat: matches 2572. ,2685 of consensus"
30005
                                                                                                   4779. .24919
note="FLAM A repeat: matches 1. .132 of consensus"
5002. .25361
note="TIMELE repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                             923. .26224
ote="AluSx repeat: matches 1. .300 of consensus"
                                                                              note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                           repeat: matches 1. .311 of consensus"
                              notes AluY repeat: matches 1. .303 of consensus
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/notes"LIPAL2 repeat: matches 912, .113 of consensus"
25036. .25335
/notes"AluY repeat: matches 301. .2 of consensus"
25338. .25826
/notes"Li repeat: matches 5356. .4861 of consensus"
27399. .3059. .3059.
/notes"Li repeat: matches 4081. .959 of consensus"
30542. .31494
/notes"Lix repeat: matches 969. .14 of consensus"
31503. .32685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187. .52286
ote="LINA9 repeat: matches 1020. .529 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 1028. .294 of consensus"
                              #159. .iff##
note="MBR4A2 repeat: matches 211. .504 of consensus"
                                                                    // noce="MIR repeat: matches 54. .114 of consensus"
[8431. .18468
// note="19 copies of 2 mer 87 % conserved"
[85958. .21148
// noce="Li repeat: matches 4197. .5387 of consensus"
[1004. .21887
// noce="Lize to the consensus"
[1004. .21887
// noce="Lize to the consensus"
[1004. .22027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      otem"MER21B repeat, matches 386. .78 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacomplete repeat: matches 5358, .4470 of consensus"
[3433. .5361
[Anote="Alusg repeat: matches 298, .103 of consensus
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te-"LiPA3 repeat: matches 889. .804 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Alugg repeat: matches 1. .96 of consensus incomplete repeat" 54510. 54571 Chote=*MEM6 repeat: matches 803. .864 of consensus" 55169. .55442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MER6 repeat: matches 865. .738 of consensus"
.52465
'note="MBR4A2 repeat: matches 1. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3882. 54095. motches 4089. 4311 of consensus" 4106. 54245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 .36401
hte="Alusq repeat: matches 1, ,303 of consensus"
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95. .40496
ste="Aluy repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    notem*Li repeat: matches 1207. .6 of consensus*
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1. .45080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oce 16 copies of 6 mer 90 % conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete repeat"
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7079. .57188
Thore="LiPAl3 repeat: matches 782. .892 of consensus"
37235. .57376
Thore="LiPAl2 repeat: matches 770. .421 of consensus"
'notes"LiMAlO repeat: matches 738. .456 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MER21B repeat: matches 388. .79 of consensus"
                                                                                                                                                                                                                                                                                                                                                           notes"L1 repeat: matches 5019. .4903 of consensus" 0234. .60527
                                                                                                                                                                                                                                                                                                                                                                                                 finctes" Alus repeat: matches 296. .1 of consensus" 10550. .61291
                                                                            note="LIMB3 repeat: matches 462. .41 of consensus"
                                                                                                                  note="L1 repeat: matches 5144. .4530 of consensus"
                                                                                                                                                                                                                                                          8511. .59531
note="LlMA2 repeat: marches 1055. .3 of consengus"
                                                                                                                                                                                                                                                                                                                       notes "L1 repeat: matches 5390. .5013 of consensus"
                                      repeat: catches 1. .426 of consensus"
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Query Match

60.6%; Score 20; DB 9; Lengtt. 118767;

Best Local Similarity 82.1%; Pred. No. 1.2e+03;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps

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Search completed: May 24, 2004, 11:40:56 Job time : 978.689 secs

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May 24, 2004, 10:22:21; Search time 1822.47 Seconds (without alignments) 540.723 Million cell updates/sec
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ALB86016 ALB86016 BX773718 BX773718 CAL43457 SCQSKT203 BM618139 170006588

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I (bases I to 727)
Vettore,A.L., da Silve,P.R., Kemper, B.L. and Arruda,P.
Genet. Mol. Biol. 24 (I-4), 1-7 (2001)
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Email: parrotachulcamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 035 row: A column: 07
Seq primer: SP6 Promoter primer.
Location/chalifiers
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                                                                                     Length 758;
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Universidade Estadual de Campinas
Caixa Postel 610, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Pax: 55 19 3788 1089
                                                                                                                                                                  Indels
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                                                                                          DB 13;
                                                                                     Query Watch 67.9%, Score 22.4, DB 13
Best Local Similarity 81.2%, Pred. No. 1.6e+02,
Marches 26, Conservative 0, Mismatches 6
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// Organism="Silurana tropicalis"
// Mol Lype="mkNp"
// Mol Lype="mkNp"
// Mol Lype="Taxon:8364"
// Lone="taxon:8364"
// Lone="t
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cDNA was oligo dT primed from Sug of poly A+ RNA from egg.

**RCORI-NOLI cut cDNA was then ligated into pCS107 with BCORI at the 5' end and NoLI at the 3' end.

5' end and NoLI at the 3' end.

Yector: pCS107, Site 1: RCORI; Site 2: NotI

HOSE: **BSCHBATChia coli XL1-blue.

LOCALION/Qualifiers
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Hinton, Cambridgeshire, CB10 16A, UK
Bmail: trop@sanger.ac.ut
Sanger Kenopus tropicalis BST project 2001
Sanger Xenopus tropicalis BST project 2001
Sequencing Economic ID: TBSG046n01.qlkT7
Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Asicn M. 2011.

BCORI.Notl cut cDNA was then ligated into pCS107 with EcoRI at the
Secori pCS107; Site 1: BCORI, Site_2: Notl
Host: BScherichis colixit-blue.
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1 (bases 1 to 758)

2 Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J. Sanger Xeropus tropicalis EST project 2001 (11_2003)

Unpublished (2003)
Sanger Treater Croning MDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dew_stage="egg"
/lab_lost="rescherichia coli XL1-blue"
/lab_lost="rescherichia coli XL1-blue"
/clone_lib="xGG-egg"
/note="Vector: pCS107; Site_l: EcoR1; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNĀ from egg.
EcoR1-NotI cut cDNA was than ligated into pCS107 with
EcoR1 at the 5' end and NotI at the 3' end"
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                                                                                                                                                                                                                                      7.517
/ Organism="8ilurana tropicalis"
/mol type="mRNA"
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/clone="TEGG030008"
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Contact: Yoshhide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), 'Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0048, Japan
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa, T., Asawa, J., Namazaki, R.,
Miyazaki, A., Murata, M., Nakawara, T., Carninci, K., Numazaki, R.,
Shiraki, T., Tsagami, M., Nakawara, N., Nomura, K., Numazaki, R.,
Shiraki, T., Tsagami, M., Waki, K., Watahiki, A., Muramateu, M.,
Shiraki, Y., Tagami, M., Waki, K., Watahiki, A., Muramateu, M.,
Shiraki, Y., Tagami, M., Waki, K., Watahiki, A., Muramateu, M.,
Shiraki, Y., Tagami, M., Waki, K., Watahiki, A., Muramateu, M.,
Shiraki, Y., Direct Submission
Computational Analysis of Pull-Length Mouse Conder Center
Sagense Sequence Analysis (RZSA) system--384-format
sequence Res. 10 (10), 1617-1630 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Rajoration Research Group in Riken
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Best Local Similarity 85.3%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0;
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/dev_stage="Adult"
/lab_hoste="hlub"*A.Gam_ad.cDNAl"
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/clone="labe"*A.Gam_ad.cDNAl"
/clone="labe"*A.Gam_ad.cDNAl
/clone=
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Clone 1730068122 5', mRNA sequence.
BY052208
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metaroa, Arthropoda; Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced suso. to Permethrin - std.
                                   17000658899386 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600447011637 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles.

1 (bases i to 284)

Holt, R.A., Lin, J.-J., Murphy, S.D., Bvans, C.A., Kraft, C.L., Charlab, R., Collins, P.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
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                                                                                                                                                                                                                                                            Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celera Genomics
45 w. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 CATGCCATCTCCGAGCAGGTCGAAGCAGCGAG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pax: 2404534580
Bmall: Moltradeclera.com
Plate: W1010046ES row: B column: 12
8eq primer: M13 Reverse.
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BM618139.1 GI:18916366
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                                                                                                                         ACCESSION
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RESULT 6 BY081398

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Missing Missing Crondata; Croniata; Vertebrata; Euteleostomi; Materia; Buthoria; Rodentia; Sciurognathi; Muridae; Murinae; Massalia; Buthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (1986) 10 3620.

RS Okazat, Y. Puruno, N. Kasukawa, T., Adachi, J., Bono, H., Kcndo, S., Nikaido, I., Osatco, N., Satto, R., Suruki, H., Yamanaka, T., Kindo, S., Caronasa, J., Caronasa, J., Caronasa, J., Schonbach, C., Gojobori, T., Saldarelli, R., Hill, D.P., Bult, C., Kindo, S., Khua, J., C., Godobach, C., Gojobori, T., Saldarelli, R., Hill, D.P., Bult, C., Godobach, C., Godori, T., Stadt, D., Brusic, V., Batalovis, Batalovis, Balsal, K.W., Balsal, A., Karach, C., Corbani, L. B., Coustins, S., Dalla, E., Dragoni, T.A., Gasi, C., Godik, M., Sader, J., Kana, J., Kawasawa, Y., Koustke, L., Varach, S., Kanai, A., Kawasi, J., W., Wackhoni, L., WcKenzie, L., Warg, B. L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Marchioni, L., Wackhoni, L., Marki, M., Maglott, D.R., Mumata, R., Okido, T., Pavan, W. J., Perca, G., Pesole, G., Petrosky, N., Fillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Sandelin, A., Schneider, C., Reed, J.C., Wangle, C.A., Secol, M. Sanda, R. Sandalin, A., Schneider, C., Walle, R. D., Wang, W. J., Sanda, J., Wangne, L., Yang, L.G., Wang, Y., Wangyisawa, M., Yangyisawa, M., Yangyisawa, M., Yang, Bayasa, J., Wangne, L., Yang, L., Yang, L., Wang, Y., Wangyisawa, M., Wangne, L., Yang, M., Waterston, R., Wasu, J., Marki, Y., Kayawa, T., Wangha, J., Wangyisawa, M., Waterston, R., Lander, E.S., Kara, A., Yasunishi, A., Sathi, A., Yoshino, M., Waterston, R., Lander, E.S., Rager, J., Milayasa, J., Wangyisawa, J., W
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BY021907 RINEN full-length enriched, mammary gland RCB-0527

Jyg-MC(B) cDNA Mus musculus cDNA clone G930019H06 5', mRNA
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Broyelopedia Project of Genome Exploration Research Group in Rikan Genomic Sciences Canter and Genome Science Laboratory in Rikan. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                           /organisms=Mus musculus"
/mol_types=mRNA."
/strains=C57BL/6J*
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/clones=Yk53031N13*
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/dev_sreges=10 days neonate*
/clones=Ibs=RIKEN full-length enriched, 10 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.4%; Score 20.6; DB 13; Length 354;
Best Local Smillarity 95.2%; Pred. No. 7.64*02;
Matches 31; Conservative 0; Mismatches 4; Indels 0,
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310 TCTTCTCCGAGCCGGTGTAAGTAGGAGA 336
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1. .354
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I (bases I to 354)

S. (kazaki, Y. Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Mikaido, I., Osato, N., Saito, R., Siruki, H., Yammaka, I., Kajadaka, T., Tomaru, Y., Rasegawa, Y., Megami, A., Schonbach, C., Golobori, T., Baldaralii, R., Hill, D.P., Bult, C., Schonbach, C., Golobori, T., Saltaralii, R., Hill, D.P., Bult, C., Schonbach, C., Corbani, L.B., Schrimi, L.M., Xanapin, A., Matsuda, H., Batalov, S., Belsel, A., Fazer, K.S., Dalla, H., Brada, M., Storiani, L.B., Corbani, L.B., Cousins, S., Dalla, H., Dargani, T.A., Flacther, C.F., Porreact, A., Fazer, K.S., Gasterland, T.A., Gariboldi, M., Gissi, C., Godzik, A., Googh, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Googh, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Mackin, J., Jarvis, E.D., Kanai, A., Kawasawa, Y., Kadziserk, R., Lyons, P.A., Maglott, D.R., Kanai, A., Karai, J.Y., Lase, Y., Lyons, P.A., Maglott, D.R., Kanai, J.W., Macchiomi, L., McKenzie, L., Wiki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Gi, D., Ramachanda, R., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Gulto, T., Ereadia, G., Pencle, R., Magnath, M., Sandellin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Wangi, L., Waller, C., Milming, L.G., Whimbaw-Poncie, A., Carrinci, P., Wang, L., Yang, L., Wanger, Y., Kang, L., Kang, L., Sakai, K., Sakai, K., Sakai, K., Lander, R., Shibada, R., Rogers, J., Briney, R. and Hayashizaki, Y., Waterston, R., Lander, R., Changawa, R., Yasunishi, A., Yashino, M., Matara, C., Shirat, Y., Sakai, K., Lander, R., L
                                                                                                                                                                                                                   BY081398 RIKEN full-length enriched, 10 days neonate thymus Mus musculus cDNA clone K630031N13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GBC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Teurumi-ku, Yokohama, Kenagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sequences Hamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1677-1630 (2000)
RIKEN integrated sequence analysis (RIGA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length CDNA encyslopedia: real-time sequence clustering for construction of a
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URL:http://genome.gsc.riken.go.jp,
Alzawa,K., Almura,T., Arakawa,T., Carninci,P., Pukuda,S.,
Hirozane,T., Arakawa,T., Itob,M., Kawai,J., Konno,H.,
Hiyazaki,A., Hurata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Warahiki,A., Muramatsu,M. and
Bayashizaki,Y. Direct Submission
Computational Analysis of Pull-Length Mouse CDNAs Compared with
    269 TCTTCTCCGAGCCGGTGTAAGTAGAGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Email: genome-resgge.riken.go.jp,

Alzawa, K., Akimura, T., Arakawa, T., Teninci, P., Fukuda, S.,

Alzawa, K., Akimura, T., Arakawa, T., Teninci, P., Fukuda, S.,

Alzawa, K., Akimura, K., Bali, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, E.,

Miyazaki, A., Palazume, N., Sasaki, D., Sato, K., Shihata, K.,

Shiraki, T., Tagami, M., Waki, K., Wachiki, A., Muramatsu, M. and

Hayabhizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with

Ruman Genome Sequences Mamm Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIERN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 175-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Repleated to Nouse Genome

Encyclopedia real-time sequence and sequenced in Nouse Genome

Encyclopedia broject of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Exploration Riken Genome Lissue etiste our explainal Research in Riken contributed to

Prepare mouse Lissues.

Please visit our web site (http://genome.gec.riken.go.jp) for

further details.
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Jyg-MC(A) cDNA Mus musculus cDNA clone G830047105 5', mRNA
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                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Science of Physical and Chemical Research (RIKEN) 1-7-22 Suchitute of Physical and Chemical Research (RIKEN) 1-7-22 Suchito-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Full and articles and articles are considered as a constant of the control of the constant of 
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| Cell line="RCB-052" Jyg-WC(B) "
| Colne lib="RIKEN full-length enriched, mammary gland
| RCB-0527 Jyg-MC(B) CDNA"
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62.4%; Score 20.6; DB 13; Length 362;
Best Local Similarity 85.2%; Pred. No. 7.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0
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/mol type="mRNA"
/db xref="taxon:10090"
/clone="G930019H06"
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                                                                                                                                                     Contact: Yoshihide Hayashizaki
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Mus musculus (house mouse)
420, 563-573 (2002)
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Exponent, N., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogand, A., Shombach, C., Odjobori, T., Bidaci, R., Promator, P., Nogalaci, R., Shombach, R., Oddinaci, R., Bidaci, R., Bidaci, R., Bidaci, R., Bidaci, R., Bidaci, R., Bidaci, R., Promator, R., Stani, M., Gariboldi, M., Gariboldi, M., Gariboldi, R., W., Edger, R., M., Gouph, J., Gariboldi, R., Manasawa, Y., Codirk, M., Gouph, J., Gariboldi, R., M., Manasawa, Y., Codirk, M., Gouph, J., Gariboldi, R., Manasawa, Y., Codirk, M., Gouph, J., Gariboldi, R., Manasawa, Y., Codirk, M., Gouph, J., Gariboldi, R., Shadidi, R., Manasawa, M., Manasawa, M.,

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BY072793
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Mammalia, Butharia, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 or 373)

Standari, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, R., Tomaru, Y., Nasagawa, Y., Nogami, A.,
Schonbach, C., Golobori, T., Baldaralli, R., Hill, D. B., Bult, C.,
Hume, D. A., Ouackenbush, J., Schrimi, L. M., Kanapin, A., Marsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. M., Sradt, D., Brusic, V.,
Chothia, C., Corban, L. B., Cousins, S., Dalla, B., Dragani, T. A.,
Pletcher, C. F., Porreet, A., Pracer, K.S., Gasateriand, T.,
Ravall, H., Kanasawa, Y., Kediterski, R.M., King, B.L., Konagay, A.,
Kurochkin, I. V., Lee Y., Lenhard, B., Lyons, P. A., Maglott, D.R.,
Maltals, L., Marchionni, L., Morkenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Ravasi, T., Reed, J.C., Reed, D.C., Ramachandran, S.,
Sandelin, A., Schneider, C., Reed, D.C., Rangela, R.D., Tomita, M.,
Sandelin, A., Schneider, C., Semple, C.A., Secou, M.,
Sandelin, A., Schneider, C., Mahlereed, C., Mang, Y., Matanabe, Y.,
Mells, C., Milming, L.G., Wilmehaw-Boris, A., Yanagisawa, M.,
Sakazume, M., Saco, K., Shiraki, T., Kawai, J., Alazawa, M.,
Sakazume, M., Saco, K., Shiraki, T., Waki, K., Kawai, J., Alazawa, K.,
Shinagawa, A., Yasuniahi, A., Hashisume, W., Moterston, R., Lander, E.S.,
Rogers, J., Binray, B. and Hayashizaki, Y.
Nalyais of the mouse transcriptome based on functional annotation
of 60,770 cull-length cDNa
                                                                                                                                                                                                                                                                                                                                           BY025872 BIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA Mus musculus cDNA clone C930033L14 5', mRNA
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Sciences Center(GSC), Yokhama Institute
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Pax: 81-45-503-9212
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URL:http://genome.gec.riken.go.jp,
Alzawa,K., Akuura,T., Arakawa,I.,
Alizawa,K., Akuura,T., Arakawa,I.,
Itob,M., Kawa,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazuma,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Pull-Length Mouse cDNAs Compared with
                                                                       Gaps
Query Match
62.4%; Score 20.6; DB 13; Length 367;
Best Local Similarity 85.2%; Pred. No. 7.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0.
                                                                                                                                                                          303 TCTTCTCCGAGCCGGTGTAAGTAGAGA 327
                                                                                                                                 5 TCTTCTCCGAGCCGGTCGAATAGTGA 31
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BY025872.1 GI:26131315
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BY025872
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
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Auman Genome Sequences Mamm. Genoms. 12, 673-677 (2001)

Normalization and subtraction of cep-trapper-selected cDMAs to prepare full-length cDMA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 155-1771 (2000)

Computer-based methods for the mouse full-length cDMA cocyclopedia: real-time sequence clustering for construction of a nonredundant cDMA library. Genome Replaced in Mouse Genome Broyclopedia Project of Genome Suploration Research Group in Riken Genomic Stiences Center and Genome Suploration Research Group in Riken Genome Genome Genome Suploration Research in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Further details.

Location/Qualifiers

172
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| feell line="RCB-0527 Jyg-MC(B)"
|/clone_lib="RKEN full-length enriched, mammary gland
| RCB-0527 Jyg-MC(B) cDNR"
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62.4%; Score 20.6; DB 13; Length 373;
Best Local Smillarity 85.2%; Pred. No. 7.8ev-02;
Matches 23; Conservative 0; Mismatches 4; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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BY072793.1 GI:26175010
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Rikaryota, Metazoa; Chordata; Craniata, Vertebrata; Suteleostomi;
Rammalia; Butheria; Rodentia; Sciurognathi; Muridae; Muzinae; Mus.

2 1 (Lases I to 373)
2 ambrowicz, B.P., Abulin, A., Remirez-Solis, R., Richter, L.J.,
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Pinch, R.A.,
Priddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huangy, M., Jahng, C.,
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Si (bases 1 to 375).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lexicon Genetics Incorporated

Jego Research Forest Drive, The Woodlands, TX 77381, USA

Randl: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

LocationQualifiers
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   Mus musculus (house mouse)
Mus musculus
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Bakazume, N., Gato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Azakawa, T., Pukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishli, Y., Itoh, M., Kagawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, W., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Haysshizaki, Y. Manlysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDAAs
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heart"
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URL:http://genome.gsc.riken.go.jp,

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Computational Analysis of Full-length Mouse CDNAs Cocpared with

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Normalization and subraction of cap-trapper selected CDNAs to

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envencing pipeline with 384 milticapillary sequencer. Genome Res.

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CDNA library was prepared and sequenced in Nouse Genome

Encyclopedia to role forme Exploration Research for prepare under to feetome Exploration Research for prepare under the sequence Exploration Research on the prepare under the sequenced and sequenced in Nouse Genome

Encyclopedia to role web site (http://genome.gec.riken.go.jp) for

further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
Physical Exploration of Physical and Chemical Research (RIKEN)
1-7-22 Suchirco-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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CDNA"
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BY011790 379 bp mRNA linear EST 06-DEC-2002 BY011790 RIKEN full-length enriched; lung RCB-0558 LLC CDNA Mus

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Okazety. Puruno, M., Kasukawa T., Adachi, J., Bomo, H., Kondo, S., Ritaido, I., Osato, N., Saito, R., Hasegawa, Y., Mogami, A., Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A., Golobori, T., Baldarelli, R., Mill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, B., Cottani, L.B., Cousins, S., Dalla, B., Dragani, T.A., Pletcher, C.P., Porrest, A., Fraer, K.S., Gaasterland, T., Gorbani, L.B., Cousins, S., Gaasterland, T., Kanasawa, N., Jackson, L.J., Jarvis, B.L., Konagaya, A., Rawali, H., Kawasawa, N., Jackson, L.J., Jarvis, B.L., Konagaya, A., Kawaji, H., Wagasaka, N., Jeckson, L.J., Jarvis, B.L., Konagaya, A., Rawaji, H., Wagasaka, N., Jeckson, L.J., Marki, Maglot, D.R., Nurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglot, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Red, J.C., Red, D.J., Raid, J., Ringashim, T., Numata, S., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandellin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandila, M., Sato, K., Shizaki, T., Waki, K., Yanagisawa, M., Yangi. L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Rakawa, T., Pukuda, S., Hara, A., Hayataki, T., Maki, K., Sandila, Y., Sato, M., Sato, K., Shizaki, T., Waki, K., Satok, L., Saton, M., Sato, K., Shizaki, T., Waki, K., Sasaki, D., Shibata, R., Sandila, M., Sato, K., Shizaki, T., Waterston, R., Imotani, R., Langawa, A., Yasaisawa, M., Yasaisawa, M., Yasaisawa, M., Yasaisawa, M., Yasaisawa, M., Yasaisawa, M., Jasawa, K., Kawat, C., Atasaisawa, M., Sato, K., Shizaki, T., Waterston, R., Imotani, M., Sato, K., Shizaki, M., Sato, K., Shizaki,
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Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Namm. Genome. 12, 673-67 (2001)

Normalization and subtraction of captrapper celected CDNAs to propare full-length CDNA libraries for rapid discovery of rew genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 34 uniticapillary sequencer. Genome Res. 10 (11), 1137-1771 (2000)
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                                                                                                                                                                                                                        Bukaryota; Metaroa, Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                               Mus musculus (house mouse)
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Raxis
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BY773596
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Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
1. (bases 1 to 391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="mammary gland"
coal line="RCB-0527 Jyg-MC(B)"
/clone_lib="RIKEN full-length enriched, mammary gland
RCB-0527 Jyg-MC(B) cDNA"
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/clone="G930043H08"
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KEYWORDS
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BY773596
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B. (bases I to 387)

R. (bases I to 387)

Riyosava, H., Yagi, K., Tomaru, Y., Hasquaya, Y., Nogani, A., Schonbach, C., Gojobori, T. Baldaralli, R., Xanaphi, A., Bult, C., Hume, D.A., Quackenbush, J., Schrim, L.M., Xanaphi, A., Maseuda, H., Batalov, S., Belsel, K.W., Ellake, J.A., Bradt, D., Bursic, V., Chothia, C., Corban, L.E., Forestrik, E., Dalla, E., Dragani, T.A., Fletcher, C., Porreet, A., Frazer, K.S., Gasterland, T., Ravalla, H., Kanasawa, Y., Redzicker, R., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lyons, P.A., Magiott, D.R., Murchin, I.V., Lee, Y., Lyons, P.A., Magiott, D.R., Maltas, E., Konagaya, A., Rurochkin, I.V., Lee, Y., Lohnard, B., Lyons, P.A., Magiott, D.R., Maltas, E., Okido, T., Pavan, W.J., Perter, G., Perter, C., Reed, J.C., Ranachand, S., Sandelin, A., Schneider, C., Semple, C.A., Secou, M., Shimada, K., Shimata, R., Wagner, L., Wahlesveld, C., Wangy, Y., Matanabe, T., Manlesseld, C., Wangy, W., Mangashim, S., Rawas, T., Read, D.C., Wangy, T., Wang, T., Wang, L., Wanglasaw, M., Saro, K., Shizat, T., Wang, L., Wangher, Y., Kanadi, Y., Kawa, J., Atawa, K., Arakawa, T., Chilling, M., Kagawa, H., Wayazaki, M., Kagawa, M., Saro, K., Shizat, T., Waterston, R., Lander, C., Shizat, Y., Sasaki, M., Kasawa, K., Shinaqawa, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, C., Wangiasaw, M., Sasaki, D., Shizat, Y., Shinaqawa, R., Shizat, Y., Shinaqawa, R., Shizat, Y., Shinadawa, K., Shizat, Y., Shinadawa, M., Saco, K., Shizat, Y., Sasaki, M., Wang,
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/tione="G730029A22"
/tione="G730029A22"
/tione="RCB-0558 LLC"
/clol line="RCB-0558 LLC"
/clone_lib="RCB-0558 LLC"
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokobama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                     further details.
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Contact: Yoshinide Rayashizati
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GEC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Telis 91-65-50-9226
Raail: genome-reseagec.riken.go.jp,
OKL:http://genome.gec.riken.go.jp,
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Miyazaki,A., Marata,M., Nakamnza,M., Nomuza,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakatume,N., Basaki,D., Sato,K., Shibeta,K.,
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genes Genome Res. 10 (10), 1617-163 (2000)
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sequencing pipeline with 384 multicapillary sequencer. Genome
Recurred Sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Youse Genome
Rnoyclopedia: real-time sequence
Exploration Research denome Exploration Research Genome
Rnoyclopedia: real-time sequence
Exploration Rnow Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Youse Genome
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OST31011 Mus musculus 1295v/Bv Mus musculus genomic clone OST31011, cG492941. GI:37257647
Wells, C., Wilming, E.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, E., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, M., Hirozane-Klainkas, T., Komo, H., Nakamura, M., Sakakame, M., Birozane-Klainkas, T., Komo, H., Nakamura, M., Arakawa, T., Phuda, B., Harak, T., Waki, K., Kawai, J., Alzawa, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Hashizume, W., Imotani, K., Ishii, Y., Shinagawa, A., Yasuuishi, A., Yoshino, M., Waterston, R., Lander, E. B., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CNNs.
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Please viuse tissues.
Please viust tour web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
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CG492941
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1 (Dases 1 to 398)

2 Okazaki, Y. Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Mikido, E., Gasto, M., Salto, R., Suruki, H., Yamanaka, I., Mikido, E., Gasto, M., Salto, R., Suruki, H., Mananka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Goldbori, T., Baldarelli, R., Hill, D.P., Bult, C., Ruyachosh, J., Schrimi, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Flecther, C. T., Porrest, A., Frazer, K.S., Gasterland, T., Gartboldi, M., Gissi, C., Godrik, A., Gough, J., Grummand, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kanadawa, Y., Kadisterski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Nanchandran, S., Randelin, A., Schneider, C., Seedle, J., Ring, B.Z., Alngwald, M., Sandelin, A., Schneider, C., Rend, J., Reid, J., Rand, S., Tandraka, Y., Sandelin, R., Magner, L., Mahlestedt, C., Mang, Y., Watanabac, Y., Verardo, R., Magner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Verardo, R., Wagner, C., Wang, Y., Watanabe, Y., Verardo, R., Wagner, C., Wang, Y., Wang, Y., Watanabe, Y., Verardo, R., Wagner, C., Wang, Y., Wang, Y., Watanabe, Y., Verardo, R., Wang, Y., W
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                                                                                                            Contact: Yoshihide Hayashiraki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokobama Institute of Genome Exploration The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-501-922
Fax: 81-45-501-9226
Fax: 81-45-503-9216
Gmail: genome-resegescriken.go.jp,
URL: http://genome.gsc.riken.go.jp,
CDNA library was prepared and sequenced in Mouse Genome
Genomic Science Center and Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frissue_type="whole body"
for_atage="17.5 days embryo"
folome lib="RIKZM full-length enriched, 17.5 days embryo
whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
further details.
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Genome Res. 13 (6B), 1273-1289 (2003)
22703353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .391
organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 TCTTCTCCGAGCCGGTGTAAGTAGAGA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TCTTCTCCGAGCCGGTCGAATAGTGA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:1009G"
/clone="L930074N12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Mus musculus
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VERSION
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BY047031
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AUTHORS
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0; Gaps

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1. (Deages I to 422)
Strunno M., Kabukawa, T., Adachi, J., Bono, H., Kondo, S., Nikado, I., Osato, N., Saito, R., Suzud, H., Yamanaka, I., Kutuno M., Kababach, C., Golobori, T., Baldaralli, R., Hill, D.P., Bult, C., Schonbach, C., Golobori, T., Baldaralli, R., Hill, D.P., Bult, C., Schonbach, C., Golobori, T., Baldaralli, R., Hill, D.P., Bult, C., Schonbach, C., Corbani, L.M., Kanapin, A., Matudda, H., Batalov, S., Baisel, K.W., Blake, J.M., Bradt, D., Brustc, W., Ghothia, C., Corbani, L.W., Farer, K.S., Gasaterland, T., Pletcher, C.F., Porregt, A., Fraer, K.S., Gasaterland, T., Karai, M., Kangi, B.L., Kanaja, A., Kawai, H., Kangi, C., Corbani, L.W., Yangi, B.L., Kanagawi, T., Karachkin, I.V., Lee, Y., Lahnard, B., Lyons, P.A., Wallott, D.S., Kanai, A., Karai, H., Karasawa, W., Jackson, I.J., Jarvis, S.D., Kanai, A., Karai, H., Karasawa, M., Jackson, I.J., Jarvis, B.D., Kanai, A., Karai, J., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Marchis, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Rawachionni, L., McKenzie, L., Miki, H., Sandelin, A., Schnaider, C., Seeple, C., Settou, M., Shimada, Y., Sandelin, A., Schnaider, C., Seeple, C., Settou, M., Shimada, Y., Wangier, W., Milling, L., Walser, M., Sandelin, A., Saco, K., Shiraki, T., Kanai, M., Saco, K., Shiraki, T., Kanai, M., Sato, K., Shiraki, T., Kanai, K., Sanaki, C., Shiraki, Y., Marayes, C., Shiraki, Y., Waki, K., Sasaki, D., Shibata, R., Shibata, R., Saraims, N., Sato, K., Shiraki, Y., Wangisawa, M., Yangi, L., Malyais of the mouse transcriptome based on functional annotation of 60,770 full-Length Edward P., Salaki, Y., Sasaki, Y., Sasaki, D., Salaki, R., Sataki, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY001675
422 bp mRNA linear EST 06-DEC-2002
87001675 RIKEN full-length enriched, 15 days embryo head Mus
musculus cDNA clone 4022405A17 5', mRNA sequence.
BY001675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Bodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
                                                                                                                                                                                                                                                                                                                    /sex="male"
/clone lib="CIT Approved Numan Gencmic Sperm Library D"
// Proper="Organ: sperm, Vector: pBeloBAC11; BAC Clones in
E-coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.4%; Score 20.6; DB 28, Length 415; Best Local Similarity 85.2%; Pred. No. 8e+02; Matches 23; Conservative 0, Mismatches 4; Indels 0
                                                                                                                                                            1. .415
/organism="Romo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plates=2004 Col=12 Row=N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 TCTCGTCACCGAGCCCGTTGAAATAGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TCTCTTCTCCGAGCCGGTCGAATAGT 29
Sequence Tagged Connector
Plate: 2004 row: N column: 12
Class: BAC ends
High quality sequence stop: 415.
Location/Qualifiers
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                                                                                                                                                                      Source
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AUTHORS
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                                                                                                                                   PEATURES
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                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinas; Mus. I (Bases i to 404).

S. Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., Gupea, A., Hansen, G., Muy. Y., Radarda, J., Finch, R.A., Priddle, C.J., Gupea, A., Hansen, G., Muy. Y., Muang, M., Jaing, C., Kay, B. W., Jr., Kipp, P., Kohlhauff, B., Ma. Z.-Q., Markesich, D., Payne, R., Porter, D. G., Olan, N., Shaw, J., Schrick, J., Shi, E.-Z., Sparks, M.J., Van Sligtenhorer, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Whi kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contact: Zambrowicz BP
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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415 bp DNA linear GSS 19-SBP-1998
HS_2004_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2004 Col*12 Row=N, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexicon Genetics Incorporated

Look Research Forest Drive, The Woodlands, TX 77381, USA

Email: material selexagen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

esscribed in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.
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High Throughput Sequencing Center
University of Washington.
401 Queen Anne Avenue North, Seattle, WA 98109, USA
1911: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell_type="embryonic stem cell"
|clone_lib="Mus musculus 1296v/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus zusculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="1295V/EV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
clone="OST31011"
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       GSS.
Mus musculus (house mouse)
Mus musculus
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G88.
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                                       SOURCE
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AQ221484
LOCUS
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AUTHORS
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          KRYWORDS
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (Bases I to 420).

Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Figgott, J., BuirandelRio, H., Buxton, B. C., Edwards, J., Pinch, R.A., Frigott, J., Guppa, A., Ransen, G., Hu, Y., Huang, M., Jaing, C., Kay, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markeadch, D., Payne, R., Potter, D.G., Olan, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparis, M.J., Van Sligtenhorst, I., Vogel, P., Malke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.

Maki kinse deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Contect: Zambrowicz BP
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**Nus musculus
**Rukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
**Rukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
**Rukaryota, Metazoa; Chordata, Sciurognathi, Muridae; Murinae, Mus.
**I (bases 1 to 43)
**Akimura,T., Arakawara,T., Carninci,P., Furuno,M., Hanagaki,T.,
**Bayerami,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
**Sato,K., Shibata,K., Sakai,C., Sakai,K., Sakazume,N.,
**Saski,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
**Saski,D., Suruki,H., Tagawa,A., Takhashi,F., Takaki,T.,
**Tomaru,A., Toya,T., Watchiki,A., Yasunishi,A.,
**RiKRK Encyclopedia of Mouse-Pull-length cDNAS (Akimura,T., et al.,
**2091**
**Ungublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB864281 RIKKN full-length enriched, RCB-0464 Meth-A cDNA Mus musculus cDNA clone G430042015 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Eambrowicz et al (Nature, 1998 Apr 9;392 (6676):608-11) Class: Gene Trap.
Location/Qualifiers
OST30401 Mus musculus 1298v/Ev Mus musculus genomic clone OST30401,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lexicon Genetics Incorporated
4000 Research Porest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 62.4%; Score 20.6; DB 29; Length 426; L Similarity 85.2%; Pred. No. 88+02; 23; Conservative 0; Mismatches 4; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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/cell_type="embryonic stem cell"
/clone_llb="Mus musculus 1298V/Ev"
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                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                       CG492510.1 GI:37256796
G88,
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BB864281.1 GI:17110491
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Matches 2
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                                                                                                                        Rail: genome-resegue.riken.go.jp,
URL:http://genome-resegue.riken.go.jp,
URL:http://genome-resegue.riken.go.jp,
Alzawa,K., Atimura,T., Arakwa,T., Carninci,P., Pukuda,S.,
Alzawa,K., Atimura,T., Arakwa,T., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Maki,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Maki,Y., Maramatsu,M., Bibbta,K.,
Chno,M., Sakai,K., Sakarume,M., Sasaki,D., Sato,K., Bibbta,K.,
Chno,M., Sakai,K., Sakarume,M., Sasaki,D., Sato,K., Bibbta,K.,
Chno,M., Sakai,K., Sakarume,M., Sasaki,D., Sato,K., Bibbta,K.,
Chno,M., Sakai,K., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse Compared with
Ruman Genome Sequence Namm. Genome. 12, 673-677 (2001)
Normalization and subtraction of captraper-selected cDNBs to
prepare full-length CDNA libraries for xapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length CDNA
encyclopedia real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research for Riken contributed to
prepare mouse tissues.

plytaion of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suthiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / crase_ryce="head"
/dev grage="15 days embryo"
/dab_host=="110a"
/clone_libs*RIKEN full-length enriched, 15 days embryo
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62.4%; Score 20.6; DB 13; Length 422;
Best Local Similarity 85.2%; Pred. No. 86+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TCTTCTCCGAGCCGGTCGAAATAGTGA 31
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/clone="4022405Al7"
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/errain="C57EL/6J"
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RESULT 20 CG492510 LOCUS

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CA576637 Linear EST 19-NOV-2002 MRNA linear EST 19-NOV-2002 MSG47G11-SN NIA Mouse Hemacopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) CDNA Library (Long) Mus musculus CDNA clone NIA:K0647G11 LimaGE:30073330 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tiesue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
| the cell origin."
| the cell origin."
| the cell origin."
| clone lib="toric CGAP Lu29"
| note="Organ: lung, Vector: pCMV-SPORT6; Site_1: Sall;
| note="Toric cloned uniforectionally. Primer: Oligo dr. library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/e-Xit-/Scal+) cDNA Library (Long)
Contact: Dawood B. Dudekula
DNA Sequencing by: Incyte Genomics, Inc.
Clona distribution: NGC clone distribution information can be
Clona distribution: NGC clone distribution information can be
Cound through the I.N.A.G.B. Consortium/LLNL ac:
http://image.llnl.gov
plate: LLNAFG z cov: a column: 16
Plate: LLNAFG z cov: a column: 16
High quality sequence stop: 428.
Location/Qualifiers
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/lab_host="DH108"
/clone_lib="NIA Mouse Hematopoietic Stem Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.4%; Score 20.6; DB 10; Length 472; Best Local Similarity 85.2%; Pred. No. 8.1e+02; Matches 23; Conservative 0; Mismatches 4; Indels 0
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/clome="NIA:K0647G11 IMAGE:3C07333C"
/fissue type="Hematopoletic Stem Cell
(Lin-/c-Kit-/Sce-1+)"
                                                                                                                                                                                                                                                        1. 472
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/strain="Caech II"
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/clone="INAQR:1592119"
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/organism="Mus musculus"
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High quality sequence stop: 489
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/scrain="C57BL/6NCr"
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Mus musculus
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIXEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIXEN)
1-7-22 Suchiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fel: 81-45-503-9226
                                                                                                                                                                                                                                                    Bmail: genome-resegac.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
URL:http://genome-gec.riken.go.jp,
Itoh, M., Yonno, H., Okasaki, Y., Muramateu, M. and Hayashizaki, Y.
Itoh, M., Konno, H., Okasaki, Y., Muramateu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cmNs to
prepare full-length cDNA libraries for respid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi, K., Pujiwake, S., Inone, K., Togawa, Y., Izawa, M., Ohara, B.,
Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
and Hayashizaki, Y., Charamateu, M., Inone, Y., Kira, A.
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Bukaryota, Metazoa, Chordata; Craniata, Vartebrata; Buteleostomi,

Bukaryota, Metazoa, Chordata; Sciurognathi; Muridae; Musinae; Mus.

1 (bases 1 to 472)

NITH-MCC http://mgc.mci.nih.gov/

Unpublished (1999)

Unpublished (1999)

Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Contact: Robert Sirausberg, Ph.D.

Email: cgapbs-remail.nih.gov

CONT Library Preparation: 116 Technologies, Inc.

CDNA Library Preparation: 116 Technologies

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
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/cell line="RCB-0464 Meth-A"
/clone_lib="RIKBN full-length enriched, RCB-0464 Meth-A
cDNA"
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Fred. No. 8e+02;
0; Mismatches 4; Indels 0:
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1. .437
/organism="Mus musculus"
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'clone="G430042015"
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Ouery Match

BBE Local Similarity

BB.4.

Conservative
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BE371463
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1. .490
/organism="Mus musculus"
/fol_type="mRNA"
/fol_type="mRNA"
/db_xref="raxon:10000"
/dev_erage="p.c. 14.5"
/db_xref="raxon:10000"
/dev_erage="p.c. 14.5"
/db_host="s. coli-DHI28 (GIBCO)"
/clone lib="Xresener ngm3 wt"
/note="Organ: pencreas; Vector: pSPORT1 (GIBCO); Site_1:
Note="Organ: pencreas; Vector: pSPORT1 (GIBCO); Site_1:
Not i; Site_2: Sal 1; The library was prepared by
Catherine 8. Lee and has not been published: The pencreas
was obtained from Gerard Gradwohl (FNAS 97 P1607-1611,
2000: The cDNA's were prepared with an oligo containing a
Not! site, and Sall linkers were added to the ends. The
inserts were cut with Not! before being cloned into the
Not! Sal attes in the vectors. This is one of two
libraries, ngm3 wt and ngm3 -/-. The wt library is in
pSPORT1, T7 promoter is 5'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG514436 496 bp DNA linear GSS 02-0CT-2003 OST302692 Mus musculus 1298v/Sv Mus musculus genomic clone CO130262, genomic survey sequence.
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
mail: metrials@lexgen.com
Gene trap sequence tag generated by 3' RACB from mouse ES cells us
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
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62.4%; Score 20.6; DB 12; Length 490;
Best Local Similarity 85.2%; Pred. No. 8.28+02;
Natches 23; Conservative 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .496
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="129SV/EV"
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   Location/Qualiflers
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CG614436
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(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)"

(note=vector: pSPORTI (Invircogen); Site_1: Sall; Site_2:
Not1; Nouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA). Intramural Research
Program, NIR (http://Jgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res
11: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (Marional
Institute on Aging, USA), Jonathan Keller (National Cancer
Institute, USA). Double-stranded cDNAs were synthesized
with an Oligo(dT) primer [Invitrogen:
5.-pGACTMGTCTGAGACGGCGCCTTTTTTTTTTTTTTTTTTT] from
1.1 ug of total RNA, treated with To DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to Lone-linker Li-Sal, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cNAs were amplified by long-range high fidelity PCR using
8x Tag polymerase (Takara) with a primer Salt-S. The
products were purified by phenol/chloroform and Centricon
100 The cDNAs were digested with Sall and Not! enzymes
and cloned into Sall/Not! site of 5990RT1 plasmid vector.
The DH108 B. coll host was transformed with the ligation
mixture by the standard chemical method. The average
insert site is about 2.2 kb. The library was constructed
by Yulan Piao (NIA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 490)
Malton, D., Brota, G., Fermutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Schmitt, A., Theising, B., Ritter, B., Ratin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R., Endocrine Pancreas Consortium
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Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
WA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pax: 617-495-8557

Bmail: dmeltom@biobp.harvard.edu

Bmail: dmeltom@biobp.harvard.edu

Bmail: dmeltom@biobp.harvard.edu

Bmail: dmeltom@biobp.harvard.edu

2000] Library was constructed by Catharine Lee DNA sequencing by:

Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce

(msrearce@mail.med.upenn.edu)

Seq primer: -40RP from Gibco

High quality sequence srop: 350.
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luganisma: Musculus"

/mol types"man"
/mol types"man;
/do xref="rancisopos"
/clone="walka: K0341806 | WadE: 30058229"
/tispus types"man;
/lab fost="walka: Man Mouse Osteoblast cand Library (Long)"
/clone lib="NIA Mouse Osteoblast cand Site 1: Sali; Site 2:
/mote="wester; page 10 for the Laboratory of Genetics,
/mote="wester; page 10 for the Laboratory of Genetics,
/motes "wester; page 10 for the Laboratory of Genetics,
/motes "wester; page 10 for the Laboratory of Genetics,
/motes "wester; page 10 for the Laboratory of Genetics,
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/motes "wester; page 10 for the Laboratory (Long)"
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/motes wester; page 10 for the Column with Sali and Not using
/motes were purified by long-range high fidelity PCR using
/motes were purified by long-range high fidelity PCR using
/motes were purified by long-range high fidelity PCR using
/motes were purified by hemol/chloroform and Centricon
/motes were purified by phenol/chloroform and cloned into Sall/Not1 site of pSpORT1 plasmid vector
/motes were purified by man site is about 3.0 kb. The library was constructed
/mixture by the grandard chemical method. The average
/mixture by the grandard chemical method. The average
/mixture by the grandard chemical method. The searge
                                                                                                                           Bukaryota; Metazoa; Chordata; Cramiata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Cramiata; Muridae; Musinae; Musin
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UI-W-BH3-att-h-12-0-UI.rl NIH BMAP M S4 Wus musculus CDNA clone
UI-W-BH3-att-h-12-0-UI 5', mRNA sequence.
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62.4%; Score 20.6; DB 14; Length 503;
Best Local Similarity 85.2%; Pred. No. 8.2e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0;
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                                                                              Mus musculus (house mouse)
Mus musculus
CAS65719
CAS65719.1 GI:25110390
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                                                                                                                                                                                                                                                                 becassing Sol by mRNA linear BST 10-OCT-2000 ux03f03.y1 Boares thymus 2NbMT Mus musculus cDNA clone immaga:1470429 5' similar to SW.GABB_MOGSE QO0420 GA BINDING PROTEIN BETA-1 CHAIN 1, mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATI-CGAP total.
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Unbublished (1997)

Other ESTS: unbilling)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-remail.nih.gov

This olone is available royalty-free through LLNL; contact the IMABE Consortium (info@image.llnl.gov) for further information.
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                                         4; Indels
      Best Local Similarity 85.2%; Pred. No. 8.2e+02; Marches 23; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality Seq primer: -40RP from Gibco High quality sequence stop: 1. iocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 retrerecasececteraagraga 192
                                                                                                                                         166 TCTTCTCCGAGCCGGTGTAAGTAGAGA 192
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clone="IMAGE:3470429"
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Mus musculus
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CG531045 S13 bp DNA linear GSS C1-OCT-2003 OST113328 Mus musculus 1298v/Ev Mus musculus genomic clone OST113328, genomic survey sequence.
                                                                                      CG530185

OST111625 Mus musculus 1298v/Bv Mus musculus genomic clone
OST111625, genomic survey sequence.
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Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pigott, J., Beltrandelkio, H., Buxton, E.C., Edwards, C., Finch, R.A., Priddle, C.J., Gupta, A., Harsen, G., Hu, Y., Khang, W., Caling, C., Rey, B.W., Tr., Kipp, P., Kohlhauff, B., Na, Z.-Q., Markesich, D., Payne, R., Petter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparke, M.J., Van Sligerahorst, I., Vogel, P., Welke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
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4000 Research Porest Diive, The Woodlands, TX 77381, USA
Email: material@dlexgen.com
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Mus musculus
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/clone lib="NH BWLP M S4"
/clone lib="NH BWLP M S4"
/clone lib="HH BWLP M S4"
/nbe="Fight M S4"
/nbe="Figh" M S4"
/nbe="Fight M S4"
/nbe=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mESTWard 1.nth.gov

CUNA Library Preparation: M.B. Soares Lab Clone distribution:

Researchers may obtain BWAP CUNA clones from RESBARCH GENETICS. It

should be noted that Bento Soares is generating a small number of

additional specialized non-redundant arrays of EMAP CDNAS whose

availability will be considered under appropriate and limited
                                                                                                                               Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Butanalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus Mamaalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Le 506; Bonaldo, M.P., Lemnon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                      Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Pax: 301 443 9890
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                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
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Seq primer: M13 Reverse.
                                                                               Mus musculus (house mouse)
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TCTTCTCCGAGCCGGTCGAATAGTGA 31

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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

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Bubarata; Butharia; Rodentia; Giurognath; Muridae; Musiculus and Easter E
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Location Genetics Incorporated

Boal: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

Gene trap sequence tag generated by 3' RACE from gene ES cells as

Gene trap sequence and (Nature. 1998 Apr 9;392 (6676):608-11)

Class: Gene Trap.
While kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz Bi
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(Lin-/c-Kit-/Sex.1+) cDNA Library (Long)*
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Enkaryotta, Metazoa; Chordata; Craniata; Vertebrata; Euteleostord;
Eukaryotta; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E. I. (bases 1 to 573)

Marra,M., Hilliar,L., Kucaba,T.; Martin,J.; Beck,C.; Wylie,T.;
Underwood,M.; Steptoe,M.; Thedeiang,B., Allen,M.; Bowers,Y.;
Underwood,M.; Steptoe,M.; Thedeiang,B., Allen,M.; Bowers,Y.;
Ritter,B.; Kobn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;
Materston,R.; and Wilson,R.

The Washb-NCI Mouse EST Project 1999
Ungublished (1999)
Other_ESTS: Allson,X.

Contact: Marra M(MashJ-NCI Mouse EST Project 1999
Washington University School of Medicine
Mashington University School of Medicine
Hat Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
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/lab host="BH108"
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/clome lib="sugano mouse embryo mouse embryo mewa"
/clome lib="sugano mouse embryo e
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ull9m07.yl Sugamo mouse embryo mewa Mus musculus cDNA clone iMAGE:2087988 5' similar to gb:M74516 Mouse GA binding protein
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/organisme"Mus musculus"
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/strain="C5781"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
West Department of Agriculture Research Service, Pacific West Area Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                               Judy A. Steen Stee
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Triticum asstivum
Triticum asstivum
Triticum asstivum
Triticum asstivum
Triticum asstivum
Triticum, Uxidiplantas, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Uxidiplantas, Itiliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
I (baceae, Triticeae, Triticum.
Anderson, 0.0., Chao, S., Chin, A., Close, T.J., Gustafson, J.P.,
Laro, G.R., Rausch, C.J., Ross, K., Sexton, C.L. and Wilson, C.
Instructure and function of the expressed portion of the wheat
Genomes - Aluminum-stressed root tip cDNA library
                  /lab_host="DH10B" close Mesenchymal Stem Cell cDNA Library (Long I)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: condergnopw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: 8K primer.
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62.4%; Score 20.6; DB 14; Length 527;
Best Local Similarity 85.2%; Pred. No. 8.3e+02;
Natches 23; Conservative 0; Mismatches 4; Indels 0;
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/moi_type="mRNA"
/cultivar="BH1146"
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dev_stage="9-15C cells"
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| organiew=Mus musculus"
| organiew=Mus musculus"
| mol_type="muscs"|
| db_xref="miscs"|
| db_xref="miscs"|
| db_xref="miscs"|
| db_xref="taxon:10090" |
| clone="NIA:80369A09 IMAGE:3043656" |
| clone="NIA:80369A09 IMAGE:30436656" |
| clone="NIA:80369A09 IMAGE:30436656" |
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Eukaryota; Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Muzinae; Mus.
1 (bases 1 to 575)
Piao,Y., Xo,N.T., Lim,N.K. and Ko,N.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD554154
B0369A09-5 NIA Mouse E9.5 Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:B0369A09 IMAGB:30435656 5', mRNA sequence.
with an oligo(dT) primer [ArGTGGCCTTTTTTTTTTTT]; double-stranded orDNA was ligated to a DralI adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pWE188-TE3 vector (5° site CACTGTGG, 3' site CACTGTGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments also. inharary constructed by Dr. Sumio Sugano (university of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer cracctcranactaccand 3' end primer
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Laboratory of Genetics
National Institutes of Health
National Institute on Aging/National Institutes of Health
313 Cassell Drive, Buite 4000, Baltimore, MD 21224-6820, USA
Bmail: classell Drive, Buita.nih.gov
Plate: B0369 row: A column: 09
Plate: B0369 row: A column: 09
High quality sequence stop: 575
POLYA-NO.
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Name Annual Metazoa, Chordata, Craniata, Vertebrata, Suteleostomi, Barkaryota, Metazoa, Chordata, Craniata, Vertebrata, Suteleostomi, Markaryota, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 Ibases 1 to 598]

13 Ibases 1 to 588]

14 Ibases 1 to 588]

15 Piao Y., Kargul, G., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.

15 Systematic Analyses of MIA Mouse Hematopoietic Stem Cell

(Lin-, C-Kit-/Gca-1+) cDNA Library (Lorg)

Unpublished (2001)

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Liboratory of Genetics

National Institute on Aging/National Institutes of Health

33. Gassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Emall: cdna@lgeun.grc.nia.nih.gov

Plate: K0617 row: B column: 04

Seq primer: M13 Revarse

High quality sequence stop: 598

POLYA=NO.
Oligo (dr) primer [Invitrogen:
5. pagaringtrcraagragedscagecoccccrrritrrrrrrrr-3']
5. pagaringtrcraagragedscagecoccccrrrrrrrrrrrrrr-3']
Erome.1 ug of total RNA, treated with 74 DNA polymerase,
and purified by ethanol-precipitation. The cDNAs were
ligated to lone-linker il-3all4, purified by
phenol/chloroform, and separated from free linkers by
Centricon 100. Then, the cDNAs were amplified by
long-range high fidelity PCR using Ex Taq polymerase
(Takara) with a primer 8al4-S. The products were purified
by phenol/chloroform and Centricon 100. The cDNAs were
digested with Sal1 and NotI enzymes and cloned into
sal1/NotI site of pCNV-SPORT6 plasmid vector. The DH10B B.
coll host was transformed with the ligation mixture by the
standard chemical method. The average insert size is about
3.0kb. The library was constructed by Yulan Plao."
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KO617B04-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)
CDNA Library (Long) Mus musculus CDNA clone NIA:K0617B04
INAGE:30070383 5', mKNA sequence.
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| Anoletype="musculus" |
| Anoletype="musus musculus" |
| Anoletype="musus musculus" |
| Anoletype="musus musculus" |
| Anoletype="musus" |
| Anole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 TCTTCTCCGAGCCGGTGTAAGTAGAGA 416
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CAS74494.1 GI:25119195
RST.
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Best Local Similarity
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Saps

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Rukaryota, Netazoa, Chordata, Craniata, Vertebrata; Buteleostomi;

Rumaalia, Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Mus.

1. (bases I to 604)

B. (bases I to 604)

B. Longacre, S. Mahmoud, M., Meenen, B., Pedersen, T.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Middehausern, A. and Wright, D., Weise, R.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

L. Onteat; Robert B. Weise

University of Utah Genome Center

Wen, 180, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
/sex="Male"
//ab host="E. Coll strain X110-Gold, T1-resistant, P-"
//clone lib="Mouse lobb plasmid UVGCM library"
//note="Vector: PMD42nv; Purified genomic DNA from N.
//note="Vector: PMD42nv; Purified genomic DNA from N.
//www.jax.org/resources/documents/dnares/). The DNA
//thtp://www.jax.org/resources/documents/dnares/). The DNA
was hydrodyramically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ365610
1M0112A19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic cone UUGCIM0112A19 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match.

62.4%; Score 20.6; DB 9; Length 599;
Best Local Similarity 85.2%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 1,000 Std Error: 0.00
Plate: 0112 row: A column: 19
Seq primer: CGTTGIAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 604.
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/mol type="genomic DNA"
/erain="c57BL/69"
/db xref="taxon:10090"
/clone="UUGCIMO112A19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 TCTTCTCCQAGCCGGTGTAAGTAGAGA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S TCTTCTCCGAGCCGGTCGAAATAGTGA 31
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Fax: 801 585 7177
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84112, USA
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A1365610
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AUTHORS
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   Extarycte, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Kammalia, Butheria, Rodentia, Sciurognathi, Muridae, Mutinae, Mus. 1 (bases 1 to 599)
Marra, M., Hillier, L., Allen, M., Bowles, M., Districh, N., Dubuque, T., Gefsel, S., Kuchae, T., Lacy, M., Lac, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Morre, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Milson, R. and Materston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA175402 599 bp mRNA linear EST 16-FEB-1997 ms80a06.rl Soares mouse 3NbwS Mus musculus cDNA clone IMAGE:617842 5. eimilar to gb:M74517 Mouse GA binding protein (MOUSE); mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macterion, M.
The WashU-HMM Mouse EST Project
Upublished (1996)
Context: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashU-HMMI Mouse EST Project
WashU-HMMI Mouse EST Project
WashU-HMMI Mouse EST Project
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WashI-HMMI 286 1800
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Fax: 316 286 1
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/organism="Mus musculus"
/organism="MRNa"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:617842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 TCTTCTCCGAGCCGGTGTAAGTAGAGA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S TCTTCTCCGAGCCGGTCGAAATAGTGA 31
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/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
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AA175402
AA175402.1 GI:1756541
BST.
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AA175402
LOCUS
DBPINITION
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AUTHORS
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Mus musculus (house mouse)
Mus musculus
Mus musculus
Mus musculus
Muscaryota, Motazao; Chordata; Craniata; Vertebrata; Ruteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 638)
Talo,Y., Ko,N.T., Lim,W.K. and Ko,M.S.H.
Construction of long-transcript enriched cDMA libraries from
submicrogram amounts of total RMAs by a universal PCR amplification
                                                                                                                                                                                        CP911216
CP911216
CP911216
CP645CO2-SNIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)
CDMA Library (Long 1) Wis misculius CDNA clone NIA:A0645C02
IMAGE:30751897 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dawcod B. Dudekula
Laboratory of Genetics
Mational Institutes of Health
Mational Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Bmail: cdna@lgeun.grc.nia.nih.gov
Bmail: cdna@lgeun.grc.nia.nih.gov
Beq pzimor: MJ Beverse
High quality sequence stop: 638
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/mol_type="mRNA"
/errain="C57BL/6NCr"
/db_xref="niaEST.A0645C02-5"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 11 (9), 1553-1558 (2001)
        287 TCTTCTCCGAGCCGGTGTAAGTAGAGA 313
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TITLE
                                                                                                                            RESULT 40
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            셤
polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored lonk was purified and size-selected for a 9.5 to 10.5 kb range using preparative selected for a 9.5 to inc.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pmn42 (gi|473114|gb|AP139172.1), a copy-umber inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-complement E. coli XLMO-Gold (Stratagene) cells and selected for ampicillin resistance.
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18 I (Dasses I to 627)

19 I (Dasses I to 627)

10 Inpublished i 1999;

11 Institutes of Health, Mammalian Gene Collection (MGC)

12 Inth-MGC http://mgc.nci.nib.gov/

13 Inth-MGC http://mgc.nci.nib.gov/

14 Institutes of Health, Mammalian Gene Collection (MGC)

15 Inth-MGC http://mgc.nci.nib.gov/

16 Inth-MGC inth-MG
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//organism="mkNa"
//mol_type="mkNa"
//strain="Czech II"
/db_xref="taxon:10090"
/clone="HMXB:3494869"
/tissue type="spontaneous tumor, metastatic to mammary.
/tissue type="spontaneous tumor, metastatic to mammary."
/tissue type="spontaneous tumor, metastatic tumor, met
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62.4%; Score 20.6; DB 10; Length 627;
Best Local Similarity 85.2%; Pred. No. 8.5e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0.
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62.4%; Score 20.6; DB 28; Length 604;
Best Local Similarity 85.2%; Pred. No. 8.5e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 TCTTCTCCGAGCCGGTGTAAGTAGAGA 248
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Mus musculus
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BE305737
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0; Gaps

4; Indels

Matches 23; Conservative 0; Mismatches

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Search completed: May 24, 2004, 12:29:49 Job cime : 1826.47 secs

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US-08-472-194A-9
May 24, 2004, 10:35:46; Search time 30.9434 Seconds (without alignments) 358.688 Willion cell updates/sec
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/ Ggn2 6/prodate/2/ina/5A_COMB.seq:*

/ Cgn2 6/prodate/2/ina/5B_COMB.seq:*

/ Cgn2 6/prodate/2/ina/6A_COMB.seq:*

/ Cgn2 6/prodate/2/ina/6B_COMB.seq:*

/ Cgn2 6/prodate/2/ina/PcTuS_COMB.seq:*

/ Cgn2 6/prodate/2/ina/PcTuS_COMB.seq:*

/ Cgn2 6/prodate/2/ina/PcTuS_COMB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-649-167A-9
US-09-849-1669-8
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US-08-42-1344-9/C

I Sequence 9, Application US/08472194A

| Rateant No. 5807718
| PAPLICANT: JOYCE, Gerald P
| APPLICANT: JOYCE, Gerald R
| ATITLE OF INVENTION: RAINTAIL DNA MOLECULES
| TITLE OF INVENTION: RAINTAILC DNA MOLECULES
| NUMBER OF SEGUENCES: 40
| CONRESPONDENCE ADDRESS:
| ADDRESSER: PREENT COUNSE!
| STREET: 10550 NO. 5807718th Torrey Pines Road, TPC 8
| CITY: La Jolla |
| STREET: 10550 NO. 5807718th Torrey Pines Road, TPC 8
| CITY: La Jolla |
| STATE: CA |
| COWFUTER: BALABLE FORM: ROADENS |
| COWPUTER: BALABLE FORM: ROADENS |
| COMPUTER: DIOPPY disk |
| SOFTANAS: Petentin Release #1.0, Version #1.25 |
| REPLICATION NUMBER: US 08/349.023 |
| PILING DATE: 07-UNH-1995 |
| RELIGATION NUMBER: TSR 463.1 |
| TELEMONE: FILLION INPORMATION: REPRENCE/DOCKET NUMBER: TSR 463.1 |
| TELEMONE: C1-784.0103 |
| TELEMONE: C1
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ALIGNMENTS
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INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS.
LENGTH: 10 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
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1 ACTCACTATAGGRAGATG 20

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Gequence 8, Application US/09849069;

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ronald R. Breaker
TITLE OF INVENTION: Bioreactive Allosteric Polymucleotides
FILE REPRENCE: OCR-94.CIP 94.019;
CURRENT APPLICATION NUMBER: US/09/849,069;
PRIOR APPLICATION NUMBER: US 09/331,809;
PRIOR PILING DATE: 1999-06-18;
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 8
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APPLICANT: ROLAIG R. Breaker
TILLS OP INVENTION: Bioreactive Allosteric Polynucleotides
FILE REFERENCE: OCR-794.CIP
FILE REPERENCE: OCR-794.CIP
CURRENT ETLING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US 09/331,809
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TILLE OF INVENTION: Bioreactive Allosteric Polynucleotides
FILE REPRENCE: OCT-794. (19.
TURERT APPLICATION NUMBER: US/09/849, D69
CURRENT FILING DATE: 2001-05-07
FRIOR PPLICATION NUMBER: US 09/331,809
FRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 53
LENGTH: 38
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100.0%; Score 20; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 20; Conservative 0; Mismatches 0
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100.0%; Score 20;
Best Local Similarity 100.0%; Pred. No. (
Matches 20; Conservative 0; Mismatch
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; OTHER INPORMATION: template, part 1
US-09-849-069-53
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US-09-849-069-53
IS-09-940-069-53
Patent No. 6630306
GENERAL INFORMATION:
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| Patent No. 6630106
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ORGANISM: artificial sequence
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US-09-849-069-8
RESULT 4
715-09-849-059-8
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                                                                                                                                                                                                                  APPLICANT: Barbas, Carlos F.
APPLICANT: Barbas, Carlos F.
APPLICANT: Santoro, Stephen W.
APPLICANT: Santoro, Stephen W.
APPLICANT: Santoro, Stephen W.
APPLICANT: Santoro, Sakthivel
TITLE OF INVENTION: BYZYMATIC DNA MOLECULES THAT CONTAIN MODIFIED
TITLE OF INVENTION: NUCLEOTIDES
FILE REPERRORS: SCR21445
CURRENT APPLICATION NUMBER: US/09/262,142B
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE OF SEQ ID NOS: 2.1
SEG ID NO 9
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: Description of Artificial Sequence: template US-09-262-142-9
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Best Local Similaricy 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0;
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APPLICANT: JOYCE, Gerald F.
APPLICANT: JOYCE, Gerald F.
APPLICANT: JOYCE, Gerald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REPERENCE: SCR.1913
CURRENT APPLICATION NUMBER: US/08/649,567A
CURRENT PILING DATE: 1997-08-25
PRIOR PILING DATE: 1995-12-01
PRIOR PILING DATE: 1995-12-01
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR PILING DATE: 1994-12-02
PRIOR APPLICATION NUMBER: 08/349,023
PRIOR PILING DATE: 1994-12-02
NUMBER: 08 SEQ 1D NOS: 101
SEQ ID NOS: 101
                                                                                                                                               Bequence 9, Application UB/09262142B; Patent No. 6110462; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bequence 9, Application US/08849567A Patent No. 6326174
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ORGANISM: Artificial Sequence
PEATURE:
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                                                                                                       RESULT 2
US-09-262-142-9/c
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APPLICANT: BALDES, CARLOS P.

APPLICANT: SALCOTO, Stephen M.

APPLICANT: SALCOTO, Stephen M.

APPLICANT: SALCOTO, Stephen M.

APPLICANT: RADISBROWY, SAKTALVEN

TITLE OF INVENTION: BUZZMATIC DNA MOLECULES THAT CONTAIN MODIFIED

TITLE OF INVENTION: NUCLECTIOES

PILE REFRENCE: SCR21448

CURRENT APPLICATION NUMBER: US/09/262,1428

CURRENT APPLICATION NUMBER: US/09/262,1428

WUMBER OF SEQ ID NOS: 58

SOPTWARE: PATENT NOST 2.1
                                                                    Sequence 11, Application US/09262142B
Sequence 11, Application US/09262142B
SEARCH, INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Sarcoro, Seraid
APPLICANT: Kandasany, Sakchivel
TITLE OF INVENTION: MUCLEOTIDES
TITLE OF INVENTION: MUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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1 OTHER INPORMATION: Description of Artificial Sequence: primer
US-09-262-141-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 20; DB 3; Length 43; Best Local Similarity 100.0%; Pred. No. 0.4; Matches 20; Conservative 0; Mismatches 0; Indele
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Best Local Similarity 100.0%; Score 20; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base
| LOCATION: (28)
| OTHER INFORMATION: adenosine ribonucleotide
US-09-262-142-13
                                                                                                                                                                                                                                                                                              PILB REPERENCE: SCR21445
CURRENT PAPLICATION NOWBER: US/09/262,142B
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 58
SOPTWARE: Patentin Ver. 2.1
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.09-262-142-13
Sequence 13, Application US/09262142B
Patent No. 6110462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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US-08-849-567A-11
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APPLICANT: Breaker, Romald F
APPLICANT: Breaker, Romald R
ATTLE OF INVENTION: ENZYMATIC DNA MOLECULES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS: 74
ADDRESSER: Patent Counsel
STREET: 10550 No. 5807118th Torrey Pines Road, TPC 8
CITY: La John
                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DB 4; Length 38; Best Local Similarity 100.0%; Pred. No. 0.39; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 29; DB 1; Length 43; Best Local Similarity 100.0%; Pred. No. 0.4; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
GOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,194A
FILING DATE: 07-UNN-1395
GLASSIPTCATION DATA:
APPLICATION NUMBER: US 08/349,023
FILING DATE: 07-UNS-1395
ATTORNEY/AGENT INPORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 154,163
REFERENCE/DOCKET NUMBER: 1581 463.1
TELECOMMINICATION INPERMATION:
TELECOMMINICATION INPERMATION:
TELECOMMINICATION INPERMATION:
TELECOMMINICATION INPERMATION:
TELECOMMINICATION INPERMATION:
TELECOMMINICATION INPERMATION:
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; Sequence 11, Application US/08472194A
; Patent No. 5807718
                                                                                                                                                                                                                                                                                                                                                                            1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                    14 ACTCACTATAGGAAGAGATG 33
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; MOLECULE TYPE: DNA (genomic)
US-08-472-194A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-784-9359
INPORMATION POR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 DASSE PATIE
                                                                                                                            TYPE: DNA ORGANISM: artificial sequence
PRIOR FILING DATE: 1999-06-18
NUMBER OF BEQ ID NOS: 57
SOFTWARE: MS-DOS
SEQ ID NO: 57
                                                                                                                                                                                                 CTHER INFORMATION: primer US-09-849-069-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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; 3equence 32, Application US/09849069; Patent No. 653036; Patent No. F630308; Patent No. Forestin No. 8 Deceative Allosteric Polynucleotides; TITLE OF INVENTION: Bloreactive Allosteric Polynucleotides; PILE OF INVENTION: BAPACIDE COLORENT APPLICATION NUMBER: US/09/849, 069; CURRENT FILING DATE: 2001-05-07; PRIOR APPLICATION NUMBER: US 09/331,809; PRIOR FILING DATE: 1999-06-18; NUMBER OF: SEQ ID NOS: 57; SEQ ID NOS: 57; LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                             APPLICANT: Ronald R. Breaker
TITLE OF INVENTION: Bioreactive Allosteric Polynucleotides
FILLS REFERENCE: 07794.C1794.C19
FILLS REFERENCE: 07794.C19
CURRENT APPLICATION NUMBER: U8/09/849,069
PRIOR APPLICATION NUMBER: U8 09/331,809
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 57
LENUMBER OF SEQ ID NOS: 57
LENUMBER OF 03
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 5807713th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 4;
Pred. No. 0.43;
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APPLICANT: Breaker, Romald R
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
HUNDER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Fred. No. 0.4
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
COTHER INFORMATION: Self-cleaving DNA
US-09-849-069-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-472-194A-13
; Sequence 13, Application US/08472:94A
; Patent No. 5807718
     Application US/09849069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: C1 variant DNA US-09-849-069-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                  TYPB: DNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-849-069-32
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Sequence 23, Application US/09262142B

Parent No. 611062

GENERAL INFORMATION:
APPLICANT: Barbas, Carlos P.
APPLICANT: Joyce, Gerald
APPLICANT: Santoro, Stephen W.
APPLICANT: Kandasamy, Sakthivel
TITLE OF INVENTION: RNZYMATIC DNA.MOLECULES THAT CONTAIN MODEFIED
TITLE OF INVENTION: NUCLEOTIDES
CURRENT PAPLICANTON: NUCLEOTIDES
CURRENT PAPLICANTON NUMBER: US/09/262,142B
CURRENT PALLIANG DATE: 1999-03-03
NUMBER OF SEQ 1D NOS: 58
SOUTHARR: Patentin Ver. 2.1
SEQ 1D NO 23
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
PRATURE:
CTHEN INFORMATION: Description of Artificial Sequence: oligomer
PRATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.04; Score 20; DB 4; Length 43; Best Local Similarity 100.04; Pred. No. 0.4; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                       APPLICANT: Breaker, Serald P.
APPLICANT: Breaker, Sonald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REPRENCE: SCRIAGAS
CURRENT APPLICATION NUMBER: 105/08/649,567A
CURRENT PILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: 08/472,194
PRIOR PILING DATE: 1995-12-01
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SEQUENALE: PRECENTIN NUMBER: 08/419,023
PRIOR PILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SEGUENALE: PRECENTIN VOY: 2.1
Sequence 11, Application US/08849567A Patent No. 6326174
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; OTHER INFORMATION: n = g, a, c or t
US-09-262-142-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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LOCATION: (49)
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US-09-849-069-33
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US-09-849-069-48
US-09-849-069-48
Sequence 48, Application US/09849069
Patent No. 6530306
GENERAL INPORATION:
TITLE OF INVENTION:
PILLE BEFERENCE: OCR-994.CIP
CURRENT APPLICATION NUMBER: US/09/849,069
CURRENT APPLICATION NUMBER: US/09/849,069
CURRENT APPLICATION NUMBER: US/09/849,069
CURRENT PLING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US/09/331,809
NUMBER OF SEQ ID NOS: 57
LENGTH: 65
LENGTH: 65
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US-08-472-1944-23

FESULT 17

Sequence 23, Application US/08472194A

FALENT NO. $807718

GENERAL INFORMATION:
MURBER NO. $807718

APPLICANT: JOYCE, Gerald F

APPLICANT: JOYCE, Gerald F

APPLICANT: BREAker, Ronald R

TITLE OF INVENTION: WAZVMATIC DNA MOLECULES

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS: 40

CORRESPONDENCES: 40

CORRESPONDENCES: 40

COUNTRY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER: IN PC COMPATIBLE

COMPUTER: BLADABLE FORM:
MEDIUM TYPE: PLORDY disk

COMPUTER: PARADABLE PORM:
MEDIUM TYPE: PLORDY ALSK

COMPUTER: BLE PC COMPATIBLE

OPERATING STREEM: PC-DOS/NS-DOS

SOFTWARE: PARADABLE

PAPLICATION NUMBER: US/08/472,194A

FILING DATE: -UW-1995

CLASSIFICATION: 536

PRIOR APPLICATION: 536

PRIOR APPLICATION DATA:
                                                                                                        Query Match 95.0%; Score 19; DB 4; Length 43; Best Local Similarity 95.0%; Pred. No. 1.2; Matches 19; Conservative 0; Mismatches 1; Indels
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1 LOCATION: 11...13
2 OTHER INPORMATION: HD2
1. OTHER INFORMATION: n is an RNA A linkage
UG-09-849-069-48
                                                                                                                                                                                                                                                    1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                      19 ACTCACTATNGGAAGAGATG 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: artificial sequence
       ; OTHER INFORMATION: substrate US-08-849-567A-13
                                                                                                                                                                                                                                                                                                                      셤
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OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
OTHER INFORMATION: at position 28 is ademosine ribonucleotide
OTHER INFORMATION: Description of Artificial Sequence: fixed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.0%; Score 19; DB 1; Length 43; Best Local Similarity 95.0%; Pred. No. 1.2; Matches 19; Conservative 0; Mismatches 1; Indels
                                              COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER RALABLE FORM:

MEDIUM TYPE: IBM PC compatible

COMFUTER: IBM PC compatible

CLASSIFICATION DATA:

RELIGIOUS APPLICATION DATA:

RELIGIOUS APPLICATION DATA:

REPRESENTION NUMBER: US 08/349,023

FILING DATE: O7-UTW-1995

RECIENTATION NUMBER: 1581 463.1

TELEROWHUNICATION INFORMATION:

TELEROWHUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAME/KEY: misc difference
LOCATION: replace(28, "")
CHER INPORMATION: /standard name= "ADENOSINE"
COTHER INFORMATION: RIBONUCLEGIDE"
US-08-472-194A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08849567A

Patent No. 622674
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: JOYCE, GERAIG F.
APPLICANT: BICENER, ROHALD R.
ITLE OF INVERTION: ENZYMATIC DNA MOLECULAS
FILLE REFERENCE: SCR19438
CURRENT PLILING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: DS7-08-25
PRIOR APPLICATION NUMBER: DC7/0895/1580
PRIOR APPLICATION NUMBER: 08/42, 194
PRIOR APPLICATION NUMBER: 08/42, 194
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/42, 194
PRIOR FILING DATE: 1995-12-02
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 13
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACTCACTATAGGAAGAGATG 20
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ORGANISM: Artificial Sequence
La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-849-567A-13
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## Sequence 7, Application U8/09262142B
## Sequence 7, Application U8/09262142B
## Sequence 7, Application U8/09262142B
## Setent No. 6110462
## Setent No. 6110462
## APPLICANT: Barban Carlos F.
## APPLICANT: Dayoe, Gerald
## APPLICANT: Andeasumy, Satthivel
## APPLICANT: Kandeasumy, Satthivel
## APPLICANT: Kandeasumy, Satthivel
## TITLE OF INVENTION: ENZYMATIC DNA MOLECULES THAT CONTAIN MODIFIED
## TITLE OF INVENTION: NUCLEOTIDES
## CINSERT APPLICATION NUMBER: US/09/262,142B
## CINSERT PELICATION NUMBER: US/09/262,142B
## SOFT OF NUMBER OF SEQ ID NOS: 58
## SEQ ID NO 7
## LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEATORS:
OTHER INFORMATION: Description of Artificial Sequence: termination
OTHER INFORMATION: sequence
                                                                                                                                                                                                                                             APPLICANT: Barbas, Carlos P.
APPLICANT: Barbas, Carlos P.
APPLICANT: Joyce, Gerald
APPLICANT: Sancoro, Stephen W.
APPLICANT: Sancoro, Stephen W.
APPLICANT: Sancoro, Stephen W.
APPLICANT: Sancoro, Stephen W.
APPLICANT: Sancoro, Statementy, Santenivel
TITLE OF INVENTION: BAZYMATIC DNA MOLECULES THAT CONTAIN MODIFIED
TITLE OF INVENTION: NUMBER: US/09/262,142B
CURRENT PILLICATION NUMBER: US/09/262,142B
CURRENT PILLICATION NUMBER: US/09/262,142B
SUPRABER OF SEQ ID NOS: 58
SOFTAMER: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.0%; Score 18; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 90.0%; Score 18; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KET: modified_base

| LOCATION: (8)

OTHER INFORMATION: adenosine ribonucleotide

US-09-162-142-2
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                                                                                                                                ; Sequence 2, Application US/09262142B; Pacent No. 6110462; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPB: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified_base LOCATION: (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-262-142-7
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ORGANISM: Artificial Sequence
PRATURE
TYPES: DNA
OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The
OTHER INFORMATION: Description of Artificial Sequence: oligomer
NAME/KEY: misc feature
LOCATION: (49)...(88)
OTHER INFORMATION: n is an equimolare mixture of G, A, T and C
US-08-849-567A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KRY: misc_difference
LOCATION: replace [38, ""]
OTHER INFORMATION: /standard name= "ADENOSINE
OTHER INFORMATION: /label= rA
OTHER INFORMATION: /label= rA
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GENERAL TROUBLION:
APPLICANT: Breaker Ronald R.
TITLE OF INVENTION: BNZTMATIC DNA MOLECULES
FILE REPERENCE: SCR19438
CURRENT PELLING DATE: 1997-08-25
FRIOR APPLICATION NUMBER: US/08/649,567A
CURRENT PELLING DATE: 1995-12-01
FRIOR APPLICATION NUMBER: DG/472,194
FRIOR PILLING DATE: 1995-12-02
FRIOR PILLING DATE: 1995-12-02
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PALENCE DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 23
LENGTH: 107
APPLICATION NUMBER: US 08/349,023
PILING DATE: 02-DEC-1994
ATTORNEY/AGENT INPORMATION:
NAME: PICLING, Thomas
REGISTRATION NUMBER: 34,163
REPRENCE/DOCKET NUMBER: 15RI 463.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870RAMION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/08849567A Patent No. 6326174 GENERAL INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 ACTCACTATNOGAAGAGATG 38
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SEQUENCE CHARACTERISTICS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: substrate
                                                                                                                                                    GENERAL INPORATION:
APPLICANT: BALDS, Carlos P.
APPLICANT: BALDS, Carlos P.
APPLICANT: SANCOF, GERALD
TITLE OP INVENTION: WUCLEOTIDES
TITLE OP INVENTION: WUCLEOTIDES
TITLE OP INVENTION: WUCLEOTIDES
CURRENT APPLICATION WURBER: U8/09/262,142B
CURRENT PILING DATE: 1999-03-03
SUPPHARE: PLEING DATE: 1999-03-03
SUPPHARE: PLEING DATE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.0%; Score 18; DB 3; Length 19; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 18; Conservative 0; Mismatches 0; Indele
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J Sequence 2, Application US/08928465

Patent No. 6204024

GENERAL INPORMATION:
APPLICANT: Romano, Joseph

TITLE OP INVENTION: CCR5 RNA Transcription Based

TITLE OP SEQUENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

STREET: 1300 Piccard Drive

CITY: Rockville

STATE: US

COUNTRY: US

COUNTRY: US
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/928,465
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: adenosine ribonuclectide
US-09-262-142-12
                                                                                         sequence 12, Application US/09262142B
Patent No. 6110462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION, 435
ATTORNEY/AGENT INFORMATION:
NAME: GOTHLEY, MATY B.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-948-7400
1 TCACTATAGGAAGAGATG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IYPB: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 301-948-9751
INPORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KRY: modified base
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TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR LINEAR
TITLES OF INVENTION: LECTHERAL AMPLIPICATION OF POLYNUCLEOTIDE SEQUENCES
FILE REFERENCE: 492692001100
CURRENT APPLICATION NUMBER: U8/09/660,877
CURRENT PILLING DATE: 22
NUMBER OF SEQ ID NOS: 22
SEGTEMAR: FARCISEQ for Windows Version 4.0
LENOTH: 60
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Patent No. 6686156
GRHERAL INFORMATION:
APPLICANT: WAITH, NUTITH
ITILE OF INVENTION: TRANSCRIPTION-BASED NUCLEIC ACID AMPLIFICATION
TITLE OF INVENTION: TRANSCRIPTION-BASED NUCLEIC ACID AMPLIFICATION
THE REFERENCE: 49269200660
CURRENT APPLICATION NUMBER: US/09/693,191B
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/213,908
PRIOR APPLICATION NUMBER: 60/213,908
PRIOR APPLICATION NUMBER: 60/213,908
PRIOR APPLICATION NUMBER: 60/217,748
PRIOR PILING DATE: 2001-03-21
SPRIOR PILING DATE: 2001-03-21
SSOFINAME: BASESKO for Windows Version 4.0
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Best Local Similarity 94.7%; Pred. No. 7.9;

Matches 18; Conservative 0; Mismatches 1; Indels
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LENGTH: 54 base pairs
TYPS: muclet caid
STRANDENNESS: single
TYPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA Oligonucleotide"
HYPOTHETICAL: NO
                                                                                                                                                                   | NAME/KEY: misc feature
| LOCATION: 1.25
| OTHER INFORMATION: /label= T7 RNA Polymera
|US-08-928-465-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09660877 Patent No. 6251639 GENERAL INFORMATION:
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ORGANISM: Synthetic primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INPORMATION: IA012b
US-09-660-877-9
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                                                                                                                                                                                                                               APPLICANT: Joyce, Gerald F
APPLICANT: Breaker, Rohald R
TITLE OF INVENTION: EXPENDENCE ON MOLECULES
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10550 No. 5807718th Torrey Pines Road, TPC 8 STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE PORM:
MEDITOTY TYPE: Ploppy disk
COMPUTER READABLE PORM:
MEDITOTY TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING STETEM: PC-DGS/MS-DOS
SOTWHERT PEDLICATION DATA:
APPLICATION NUMBER: US/08/472,194A
FILING DATE: 07-VUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/349,023
FILING DATE: 02-DEC-1994
ATTORNET/AGBNT INFORMATION:
NAME: Pitting, Thomas
REGISTRATION NUMBER: 34,163
RESERRENCATION NUMBER: 34,163
RESERRENCATION NUMBER: 1581 463.1
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
TELEBCOMMUNICATION INFORMATION:
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LOCATION: replace(%, "")
OTHER INFORMATION: /standard_name= "ADENOSINE
OTHER INFORMATION: RIBONICLEOTIDE"
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Best Local Similarity 94.4%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches
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APPLICANT: Breaker; Ronald R
TITLE OF INVENTION: ENZYMATIC DNA MCLECULES
WUMBER OF SEQUENCES: 40
                                                                                                                                                      | Sequence 7, Application US/08472194A | Patent No. 5807718 | GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 12, Application US/08472194A; Patent No. 5807718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: 619-784-9399
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 19 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: . nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09660877

Parent No. 6251639

FAGRERAL INFORMATION:
APPLICANT: NULL, N.
APPLICANT: 492692000.00

CURRENT APPLICATION NUMBER: US/09/660,877

CURRENT PILING DATE: 2000-09-13

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PASESEQ for Windows Version 4.0

SEG ID NO.
APPLICANT: 67
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Sequence 11, Application US/09893191B

Parent No. 6686156

GENERAL INPORMATION:
PAPLICANT: KULT, NUTITH

TITLE OF INVENTION: PETHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: PETHODS AND COMPOSITION FOR

FILE REPREZENCE: 492692000606

CURRENT APPLICATION NUMBER: US/09/893,191B

PRIOR PILING DATE: 2001-06-26

PRIOR PILING DATE: 2001-06-26

PRIOR PILING DATE: 2001-06-26

PRIOR PILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FasteREQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 67
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seps
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                                                                                                                   DB 4; Length 60;
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87.0%; Score 17.4; DB 3; Length 67;

Best Local Similarity 94.7%; Pred. No. 8.1;

Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 87.0%; Score 17.4; DB 4; Length 67; Best Local Similarity 94.7%; Pred. No. 8.1; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                    Indele
                                                                                                                 Query Match
Best Local Similarity 94.7%; Pred. No. 8;
Matches 18; Conservative 0; Mismatches
                                           ) OTHER INFORMATION: Synthetic Primer: IA012b
US-09-893-1918-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRATURE:
POTHER INFORMATION: Synthetic Primer: IA012
US-09-893-1918-11
                                                                                                                                                                                                                                             8 ACTCACTATAGGGAGAGAT 26
                                                                                                                                                                                                                  1 ACTCACTATAGGAAGAGAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 ACTCACTATAGGGAGAGAT 33
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Synthetic primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
CTHER INFORMATION: IA012
US-09-660-877-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
US-09-893-1918-11
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US-09-660-877-8
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Sequence 38, Application US/08549211

Factor No. 587450

GENERAL INPORMATION:
APPLICANT: CLEUZIAT, Philippe
APPLICANT: GIVILOU-BUNNICT, Francoise
APPLICANT: GUILOU-BUNNICT, Francoise
APPLICANT: LEVASSEUR, Pierre
APPLICANT: MALERT, Francoise
APPLICANT: ALENTION: OLICONUCLEOTIDE WHICH CAN BE USED AS
TITLE OF INVENTION: ACCOMPANIED BY STRAND DISPLACEMENT
INVERSE ON A REPLICATION
MUMBER OF SEQUENCES:
ADDRESSES:
ADDRESSES:
ADDRESSES: Oliff & Berridge
GTRBET: 700 GOULH Washington Street, Suite 300
GTRBET: 700 GOULH Washington Street, Suite 300
GTRFET: VIEGHIS
COUNTRY: USGAILS
ZEP: Z2314
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
        PRATURE:

OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The n other INFORMATION: at position 8 is adenosine ribonucleotide.

OTHER INFORMATION: Description of Artificial Sequence: substrate US-08-849-557A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Combined DNA/RNA Molecule: The porter information: at position 8 is adenosine ribonucleotide. CHER INFORMATION: Description of Artificial Sequence: substrate 08-08-849-5678-12
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                                                                                                                                                         Query Match 85.0%; Score 17; DB 4; Length 19; Best Local Similarity 94.4%; Pred. No. 11; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 85.0%; Score 17; DB 4; Length 19; Best Local Similarity 94.4%; Pred. No. 11; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                         3 TCACTATAGGAAGATG 20
                                                                                                                                                                                                                                                                                                             1 TCACTATNOCAACAGATG 18
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Best Local Similarity 94.44; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 1; Indels
CORRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Research Institute, Office of ADDRESSES: Patent Counse!
STREET: 10550 No. 5807718th Torrey Pines Road, TPC 8
STATE: CA
                                                                                                                                                                             COMPUTER READABLE FORM,
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PRESENT PC-DOS/MS-DOS
SOTTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA: US/OS/472,194A
FILING DATE: 0.7-UM-1995
CLASSIFICATION NOWBER: US OS/349,023
FILING DATE: 0.2-DEC-1994
ATTORNEY/AGRATION NOWBER: 34,163
REGISTRATION NOWBER: 34,163
RETERMONS PARENTINGER: 7581 463.1
TELECOMMUNICATION INFORMATION:
TELEPAN: 619-784-9399
INFORMATION POR EEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TELEPAN: 19 base pairs
TELEPAN: 11 linear
MOLECULE TYPE: DNA (genomic)
FRANCHER: DNA (genomic)
FRANCHER: DNA (genomic)
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LOCATION: replace(8, "")
OTHEN INPONANTION: /standard_name= "ADENOSINE
OTHER INPONANTION: RIBONUCLEOTIDE"
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Sequence No. 6326174
GENERAL INFORMATION:
APPLICANT: JOYCE, Gerald F.
APPLICANT: JOYCE, Gerald R.
TITLE OF INVENTION: ENTYMATIC DNA MOLECULES
FILE REFERENCE: SCR19438
CURRENT PILING DATE: 1997-08-25
CURRENT PILING DATE: 1997-08-25
FRIOR PELING DATE: 1995-06-07
FRIOR PILING DATE: 1995-06-07
FRIOR PILING DATE: 1995-06-07
FRIOR APPLICATION NUMBER: 08/472,194
FRIOR PILING DATE: 1994-12-02
FRIOR APPLICATION NUMBER: 08/349,023
FRIOR PILING DATE: 1994-12-02
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US-08-849-567A-7
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Gaps
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Best Local Similarity 90.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 2; Indels
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84.0%; Score 16.8; DB 2; Length 44;
Best Local Similarity 90.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Morris, Macdonald S.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
TOTRES OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Cocpatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION: NUMBER: US 08/143,312
CLASSIPICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION: NUMBER: US 08/082,937
PRILING DATE: 25-OCT-1993
CTASSIPICATION: DATA:
APPLICATION: NUMBER: US 08/082,937
PRILING DATE: 35-OTM-1993
ATTORNEY AGENT: INFORMATION:
NAME: Liebeschuetz, Joseph O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REPERENCE/DOCKET NUMBER: 018547-204160US
TELECHOUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/08441887A Patent No. 5837832 GENERAL INFORMATION:
                                                                                                                                                                                                               1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                               13 ACTCACTATAGGGAGAGCTG 32
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MOLECULE TYPE: DNA (probe)
US-08-441-887A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAK: 650-326-2422
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           TOPOLOGY: linear
HOLECULE TYPE: DNA
US-09-015-876-23
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Patent No. H001815

GENERAL INFORMATION:
APPLICANT: ROWAND
APPLICANT: BHURTLIFF, ROXANNE
APPLICANT: BHURTLIFF, ROXANNE
APPLICANT: BHURTLIFF, ROXANNE
APPLICANT: BHURTLIPF, ROXANNE
APPLICANT: BOT INTEREST
APPLICANT OF HILV II
STREET: 1300 PICCAND DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARTLAND
COUNTRY: US
ZIP: 2005T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2, Length 40;
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COMPUTER READABLE FORM:

WEDDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT REPLICATION DATA:
FILING DATE: 27-OCT-1995
CLASSIPICATION: 435
ATTORNEY/ARRY INPORBATION:
NAME: BETTINGG: William P.
REGISTRATION NUMBER: 30,024
REFERRANCE/DOCKET NUMBER: WPB 36705
TELECHMUNICATION INPORMATION:
TELECHMUNICATION INPORMATION:
TELECHMUNICATION INPORMATION:
TELECHMUNICATION INPORMATION:
TELECHMUNICATION INPORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC COMS/MS-DOS
SOFTWARE: ParentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,876
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

Best Local Similarity 90.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches
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ATTORNEY/AGENT INPORMATION:
NAME: KLESNER, SHARON N
REGISTRATION NUMBER: 36,335
REFRENCE/DOCKET NUMBER: T/98353
TELEPHONE: 301-948-7400
TELEPHONE: 301-948-751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECTLE TYPE: DNA (genomic)
US-08-549-211-38
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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APPLICANT: Wangen, Inc.
APPLICANT: Wangen, Inc.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Weidenhammer, Elaine M.
APPLICANT: Xu, Xiao
APPLICANT: Xu, Xiao
APPLICANT: Kell, Brenda F.
TITLE OP INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC KI
FILE REPERBNCS: 256/262 Patrick S. Eagleman
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID MOS: 73
SOFTHARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, Xiao
APPLICANTON: ALAIN Beneda T.
FILL OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MICCORRENT PLLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 09/710,200
PRIOR PLING DATE: 2000-110-10
SOSTWARE: PATENTING DATE: 2000-11-09
SOSTWARE: PATENTING DATE: 2000-11-09
SOSTWARE: PATENTIN VEFSION 3.1
SUBJECTION NUMBER: 09/710,200
AUTHOR OF SIGN NOS: 73
LENGTH: 04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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; Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                        Sequence 4, Application US/09710200
Patent No. 6379897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09975408
Patent No. 6497122
GENERAL INFORMATION:
       8 ACTCACTATAGGGAGACATG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ACTCACTATAGGGAGAGCTG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified base

LCCATION: (1)...(1)

OTHER INFORMATION: Biotinylated
US-09-710-200-4
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; OTHER INPORMATION: Biotinylated
US-09-975-408-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                             APPLICANT: Cronin, Meureen T.
APPLICANT: Miyada Charles Garrett
APPLICANT: Miyada Charles Garrett
APPLICANT: Chee, Mark
APPLICANT: Chee, Mark
APPLICANT: Hung, Xiachua C.
APPLICANT: Lippehurz, Robert J.
APPLICANT: Mortis, Macdonald S.
APPLICANT: Sheldon, Edward L.
APPLICANT: Sheldon, Edward Conter, Sth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 84.0%; Score 16.8; DB 3; Length 44; Best Local Similarity 90.0%; Pred. No. 15; Matches 18; Conservative 0; Mismatches 2; Indels
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ZID: COMPUTER REALBELS PORM:
PEDIUM TYPE: 190Ppy disk
COMPUTER: 180 PC compatible
COMPUTER: 180 PC compatible
COMPUTER: 180 PC compatible
COMPUTER: 180 PC compatible
COMPANTING SYSTEM: PC-DCS/MG-DCS
SOFTWARE: 180 PC-DCS/MG-DCS
SOFTWARE: 180 PC-DCS/MG-DCS
SOFTWARE: 180 PC-DCS/MG-DCS
SOFTWARE: 180 PC-TOSS/MG-DCS
FILING DATE: 180 PC-TOSS/MG-DCS
PRICE APPLICATION NUMBER: US 08/510,521
PRICE APPLICATION NUMBER: PCT/US94/12305
PRICE APPLICATION NUMBER: US 08/284,064
PRICE APPLICATION NUMBER: US 08/143,312
PRICE DATE: 26-OCT-1994
PRICE DATE: 26-OCT-1993
PRICE DATE: 26-DCT-1993
PRICE DATE: 26-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   018547-004130US
                                                                                                                                                                                                                       sequence 121, Application US/08544381B
Patent No. 6027880
1 ACTCACTATAGGAAGAGATG 20
                                                                  8 ACTCACTATAGGGAGACATG 27
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REGISTATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 0185.
TELECOMUNICATION INPORMATION:
TELEPHONE: 415-576-0300
INPORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
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STRANDEDNESS: single
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1 ACTCACTATAGGAAGATG 20

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1 ACTCACTATAGGAAGAGATG 20

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TILE OF INVENTION: WULTPLEX AMPLIFICATION AND SEPARATION OF NUCLEIC ACID TILE OF INVENTION: WULTPLEX AMPLIFICATION AND SEPARATION OF NUCLEIC ACID TITLE OF INVENTION: SEQUENCES ON A BIOGENECIRONIC MICROCHIP USING ASYMMETRIC TITLE OF INVENTION: STRUCTURES

PILE REPRESENCE: 241/109

CURRENT APPLICATION NUMBER: US/09/290,452

CURRENT PILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PRECESS for Windows Version 3.0

SEQ ID NO 16

INSTANCE: SO

TYPE: ....
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Best Local Similarity 90.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Nerenberg, Michael I.
APPLICANT: Remain, Call F.
APPLICANT: Edmain, Call F.
TILLE OF INVENTION: BLECTRONICALLY MEDIATED NUCLEIC ACID
TITLE OF INVENTION: AMPLIFICATION IN NASBA
FILE REFERENCE: 238/072
CURRENT APPLICATION NUMBER: US/09/290,338
CURRENT APPLICATION NUMBER: 1999-04-12
NUMBER FILING INS: 62
SOUTWARE: PastSEG for Windows Version 3.0
SERVICE F. SECOLULY NOT SECOLULY NUMBER: PastSEG for Windows Version 3.0
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Best Local Similarity 90.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: human T-cell leukemia virus-1
US-09-290-452-16
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; ORGANISM: human T-cell leukemia virus-1
US-09-290-338-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 24, 2004, 12:31:18
Job time : 31.9434 secs
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1 Sequence 16, Application US/09290338
1 Patent No. 6326173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACTCACTATAGGAAGAGATG 20
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Patent No. 623868

GRERAL INPORMATION:
APPLICANT Carrino, John J.
TILLS OF INVENTION: MULTIPLEX APPLICATION AND SEPARATION OF NUCLBIC TILLS OF INVENTION: DISPLACEMENT AMPLIFICATION AND BIOBLECTRONIC CHIP TILLS OF INVENTION: IECHNOLOGY
FILLS REPERRACE: 238/238
CURRENT APPLICATION NUMBER: US/09/290,577
CURRENT PILLNG DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 62
SUSTIMALE PREISE FREESO for Windows Version 3.0
SEQ ID NO 16
LENGTH: 50
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                                                                                                                                                                                  APPLICANT: Cudahoorn, Pieter
APPLICANT: Kiacer, Paul
TITLE OP INVENTION: BP-TU MRNA AS A MARKER FOR VIABILITY OP BACTERIA
FILE REPERINCE: 9250.21
CURRENT APPLICATION NUMBER: US/09/600,770A
CURRENT PILING DATE: 2000-07-21
PRIOR PILING DATE: 1999-01-19
NUMBER OF EEQ ID NOS: 95
SOFTWARE: Pacentin version 3.0
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRATURE:
| NAME/KEY: misc_feature
| LOCATION: (1) ... (49)
| CTHER INPORMATION: Oligonucleotide primer to Escherichia coli EF-Tu.
US-09-600-770A-5
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Best Local Similarity 90.0%; Pred. No. 15;

Matches 18; Conservative 0; Mismatches 2; Indela
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; ORGANISM: human T-cell leukemia virus-1
US-09-290-577-16
                                                                                                                       Sequence 5, Application UB/09600770A; Patent No. 6489110; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09290452 Patent No. 6309833 GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ACTCACTATAGGGAGAGCTG 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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US-09-290-452-16
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Query Match
100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-:44-679-11
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                                                                                                                                                                                                             (without alignments) 752.721 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, M. Sequence 11, Bequence 11, Bequence 2, M. Sequence 11, Bequence 4, M. Sequence 4, M. Sequence 13, Sequence 13, Sequence 13, Sequence 13, Sequence 12, Sequence 6, M. Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                              May 24, 2004, 11:41:02 ; Search time 120.755 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (cgn2_6/prodata/1/pubpa/0807_PUBCOMB.seq:*
(cgn2_6/prodata/1/pubpa/PCT_NBW_PUB.seq:*
(cgn2_6/prodata/1/pubpa/PCT_NBW_PUB.seq:*
(cgn2_6/prodata/1/pubpa/U806_NBW_PUB.seq:*
(cgn2_6/prodata/1/pubpa/U807_NBW_PUB.seq:*
(cgn2_6/prodata/1/pubpa/U807_NBW_PUB.seq:*
(cgn2_6/prodata/1/pubpa/NBW_PUB.seq:*
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(cgn2_6/prodata/1/pubpa/U809_NBW_PUB.seq:*
(cgn2_6/prodata/1/pubpa/U8108_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-144-679-11

US-10-144-094-2

US-10-144-094-11

US-10-144-094-81

US-10-144-679-4

US-10-144-679-4

US-10-144-679-4

US-10-144-679-85

US-10-144-679-85

US-10-144-679-85

US-10-144-679-85

US-10-144-679-85

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US-10-144-679-85

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US-10-144-679-85
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                                                                                                                nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poet-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                               1 actcactataggaagatg 20
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                        US-10-144-679-2
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Match
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                              Run on:
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No.
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) OTHER INFORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric ; OTHER INFORMATION: substrate US-10-144-679-2
             Sequence 83, Appl
Sequence 79, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 92, Appl
Sequence 84, Appl
Sequence 84, Appl
Sequence 121, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 66, Appl
Sequence 56, Appl
Sequence 18, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric OTHER INFORMATION: substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10144679

Pablication No. USZ0030215810A1

GENERAL INPOSENTION:

APPLICANT: LIU, VI

APPLICANT: LIU, JUENEN

TITLE OF INVENTION: SCLORE

TITLE OF INVENTION: CCLORE

TITLE OF INVENTION: UNDERR: US/10/144,679

CURRENT APPLICATION NUMBER: US/10/144,679

CURRENT PILING DATE: 202-05-10

NUMBER: OF SEQ ID NOS: 88

SOFTWARE: PATENTIN VET: 2.1
ALIGNMENTS
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FEATURE:
7 OTHER INPORMATION: Description of Combined DNA/RNA Molecule: Synthetic chizeric CVIER INFORMATION: substrate
19-10-144-094-2
                                                                                                                                                                                                                                               PENTURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric OTHER INFORMATION: substrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels
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Publication No. US20040023216A1

GENERAL INFORMATION:

APPLICANT: LIU, YI

APPLICANT: LIU, YI

APPLICANT: LIU, YI

TILE OF INVERTION: NEW FILORESCENCE BASED BIOSENSOR

FILE REFERENCE: 10322/44

CURRENT FILIG DAITE: 2002-05-10

NUMBER OF EEQ ID NOS: 84

SOFTWARE: Patentin Var. 2.1

SEQ ID NO: 1

LENGTH: 20
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APPLICANT: U. V. VIDNERM
APPLICANT: U. V. VIDNERM
TITLE OF INVESTICATION: NEW FLUCHESCENCE BASED BIOSENSOR
FILE REFERENCE: 10322/44
FILE REFERENCE: 10322/44
CURRENT APPLICATION NUMBER: US/10/144,094
CURRENT FILLING DATE: 202-05-10
NUMBER OF SEQ ID NOS: 84
SUDTWARF PREDEILIN VEY: 2.1
ERNOTH: 20
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100.0%; Score 20; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0;
                                 CURRENT APPLICATION NUMBER: US/10/144,094
CURRENT PILING BATHS: 2002-05-10
NUMBER OF SEQ ID NOS: 84
SOPTWARE: PACENCIN Ver. 2.1
SOPTWARE: 20
LENGTH: 20
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ORGANISM: Artificial Sequence
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OTHER INPORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric OTHER INFORMATION: substrate
US-10-144-679-81
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| Sequence 81, Application US/10144679
| Sequence 82, Application No. US20330215810A1
| Sequence 84, Application No. US20330215810A1
| Septence 84, Application No. US20330215810A1
| APPLICANT: LU, VUENEN
| TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORE FOR IONS BASED ON TITLE OF INVENTION: COLCA CANAGES
| TURRENT FILING DATE: 2002-05-10
| NUMBER: OF EEQ ID NOS: 88
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 81
| LENGTH: 20
| TYPE: DNA |
| CORGANISM: Artificial Sequence
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TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON
TITLE OF INVENTION: COLOR CHANGES
FILE REPERENCE: 3800240-0019
CUTRENT APPLICATION NUMBER: US/10/144,679
CUTRENT PILLO DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 88
SSOTWARE: PACENTIN Ver. 2.1
SEQ ID NO 11
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. OTHER INPORMATION: Description of Artificial Sequence: Synthetic of OTHER INPORMATION: Rh-17DDS
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100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels
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100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels
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Publication No. U620040023216A1
GENERAL INPORMATION:
APPLICANT: LU, JUENEN
ITLE OF INVENTION: NEW FLUORESCENCE BASED BIOSERSOR
Sequence 11, Application US/10144679
Publication No. US20030215810A1
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ORGANISM: Artificial Sequence
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U9-10-144-094-13
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Bublication Wo. U820040023216A1

GENERAL INPORMATION:
APPLICANT: LIU, YI
APPLICANT: LIU, JUENEN

IIILE REPERENCE: 10122/44

CURRENT APPLICATION NUMBER: US/10/144,094

CURRENT PILLING DATE: 2002-05-10

NUMBER OF SEQ ID NOS: 84

SOFTWARE: DATE

SEQ ID NO 4

SEQ ID NO 4
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APPLICANT: LU, YIUNEN
FILLE POR INVENTION: NEW FLUORESCENCE BASED BIOSENSOR
FILLE REPERBNCE: 10322/4
CURRENT APPLICATION WURBER: US/10/144, D94
CURRENT PILLEG DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 84
SEQ ID NO 13
LENGTH: 43
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0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 1.5
Matches 20; Conservative 0; Mismatches
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US-10-144-094-13
Sequence 13, Application US/10144094
; Enblication No. US20040023216A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
20, Conservative
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                                                          PRATURE:
OTHER INPORMATION: Description of Combined DNA/RNA Molecule: Synthetic chimeric
OTHER INPORMATION: substrate
US-10-144-094-81
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                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic chimeric OTHER INFORMATION: substrate
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APPLICANT: LU, JUZHEN
APPLICANT: LIU, JUZHEN
TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON
TITLE OF INVENTION: COLOR CHANGES
FILE REPERENCE: 9800240-0019
CURRENT APPLICATION NUMBER: US/10/144,679
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ 1D NOS: 88
SOPTUMER: PATENTIN VET. 2.1
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TITLE OF INVENTION: SIMPLE CATALYTIC DNA BIOSENSORS FOR IONS BASED ON
TITLE OF INVENTION: COLOR CHANGES
FILE REPRENCE: 9800240-0019
CURRENT PAPLICATION NUMBER: US/10/144,679
CURRENT PILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 88
SOFFWARE: Patentin Ver. 2.1
LENGTH: 43
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PRATURE:
PRESTURE:
GENER INFORMATION: Description of Artificial Sequence: Primer
UB-10-144-679-4
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100.0%; Boore 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 20; Conservative 0; Mismatches 0; Indels
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Pred. No. 1.9;
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US-10-144-679-13
US-10-144-679-13
Sequence 13, Application US/10144679
Publication No. US20030215810A1
GENERAL INPORMATION:
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Publication No. US20030215810A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
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Per Lichn's Bristol-Myers Squibb Compary

TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN FOTASSIUM CHANNEL BETA-SUBUR

TITLE OF INVENTION: FOLYNUCLEOTIDE ENCODING A NOVEL HUMAN FOTASSIUM CHANNEL BETA-SUBUR

TITLE OF INVENTION: Table and the content of the current application whomen: us/10/056,884

CURRENT PILING DATE: 2002-01-24

FRIOR PILING DATE: 2001-02-14

RIOR FILING DATE: 2001-02-14

RIOR FILING DATE: 2001-02-14

ROUNGER OF EXC IN VOREE: 13

SOFTWARE: Patentin Version 3.0

SEQ ID NO 72
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TITLE OF INVENTION: POLYNCLEOTIDE ENCODING A NOVE: HUMAN POTASSIUM CHANNEL BETA-SUBUN
TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
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Best Local Similarity 90.0%; Pred. No. 87; Length 48;
Matches 18; Conservative 0; Mismatches 2; Indels
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Publication No. US20030032786A1
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LOCATION: (1) (1)
COTHER INFORMATION: Biotinylated
US-10-075-579-4
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Best Local Similarity 90.0%;
Matches 18; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: IMPROVED METHODS POR GENE EXPRESSION MONITORING ON SIECTRONIC MIC
PILE REPRENCE: 267/174 Patrick B. Bagleman
CURRENT APPLICATION NUMBER: US/09/975,408
CURRENT APPLICATION NUMBER: 09/710,200
PRIOR PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin Version 3.1
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Best Local Similarity 90.0%; Pred. No. 86;

Matches 18; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                           APPLICATION NUMBER: US 08/284,064
PILING DATE: 02-AUG-1994
APPLICATION NUMBER: US 08/143,312
PILING DATE: 46-OCT-1993
ATTORNET/AGET: INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
TELEBRONE: 415-576-0200
                                            APPLICATION NUMBER: PCT/US94/12305
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Ilinear NOLECULE TYPE: DNA (primer);
SEQUENCE DESCRIPTION: SEQ ID NO: 121: US-09-510-378-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09975408
Patent No. US20020150917A1
GENERAL INFORMATION:
APPLICANT: Wangen, Inc.
APPLICANT: Weldenhammer, Blaine M.
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Publication No. US20020119484A1
GENERAL INFORMATION:
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CTHER INFORMATION: Biotinylated US-09-975-408-4
                                                                                                                                                                                                                                                                                    TELEPAY: 415-576-0300
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERIZES:
LENGTH: 44 base paire
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ORGANISM: Homo sapiens
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US-10-075-579-4
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Gape

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Query Match

84.0%; Score 16.8; DB 15; Length 48;
Best Local Similarity 90.0%; Pred. No. 87;
Matches 18; Conservative 0; Mismatches 2; Indels 0
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Job time : 120.755 secs
                                                       ; TYPE: DNA; Drosophila melanogaster US-10-071-458-33
                                                                                                                                                                                                                                                        1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                               12 ACTCACTATAGGGAGACATG 31
           SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application U8/10086156
Publication No. U620030054989A1
GENERAL INFORMATION
TITLE OF INVENTION: FOLYNCLEOTIDE ENCODING TWO NOVEL HUMAN PUTASSIUM CHANNEL BETA-9D
FILE REPERENCE: D0115MP
CURRENT PFELICATION NUMBER: US/10/086,156
PRIOR PILING DATE: 2002-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-38
PRIOR PILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 98
SUPTIME: 2001-03-03
SUPTIME: Patentin version 3.0
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bristol-1994es Squibb Company
TITLE OF INVENTION: POLYNCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
TITLE OF INVENTION: POLYNCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBU
TITLE OF INVENTION: K+betaM3
FILE OF INVENTION: K+betaM3
FILE REPERCE: D0114 np
CURRENT APPLICATION NUMBER: US/10/071,458
CURRENT PILING DATE: 2002-02-07
FRIOR PILING DATE: 2001-02-05
FRIOR PALICATION NUMBER: US 60/267,039
FRIOR APPLICATION NUMBER: US 60/281,224
FRIOR APPLICATION NUMBER: US 60/281,224
FRIOR PILING DATE: 2001-04-03
NUMBER OF SEQ ID MOS: 76
SOFTWARE: Patentin version 3.0
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84.04; Score 16.8; D

Best Local Similarity 90.04; Pred. No. 87;
Matches 18; Conservative 0; Mismatches
FILE REFERENCE, DOIZ1 NP
CURRENT APPLICATION NUMBER: US/10/080,980
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/270,132
PRIOR APPLICATION NUMBER: US 60/270,132
PRIOR PLING DATE: 2001-03-21
PRIOR PLING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 74
NUMBER OF SEQ ID NOS: 74
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-080-980-73
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Publication No. US20030114371A1
GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster
U3-10-086-156-56
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US-10-071-458-33
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us-10-144-679-2.rge

Copyright (c) 1993 - 2004 Comparen Ltd.

Copyright (c) 1993 - 2004 Comparen Ltd.

Run on: May 24, 2004, 10:18:57; Search time \$93.811 Seconds
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Run on: May 24, 2004, 10:18:57; Search time \$93.811 Seconds

Run on: May 24, 2004, 10:18:57; Search time \$93.811 Seconds

Scoring table: 10:10-144-679-2

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Minimum D9 seq lampth: 20:00:00:00

Reading may be a set seffying chosen parameters: 6340544

Minimum D9 seq lampth: 20:00:00:00

Reading Minimum Match 104

Minimum D9 seq lampth: 20:00:00:00

Reading Minimum Match 104

Listing first 45 summaries

Database: 11:00-10:00

Searched: 11:00-10:00

Searched: 12:00-10:00

Listing first 45 summaries

Database: 11:00-10:00

Searched: 12:00-10:00

Searched: 13:00-10:00

Searched: 14:00-10:00

Searched: 15:00-10:00

Searched: 16:00-10:00

Maximum Match 104

Listing first 45 summaries

Database: 10:00-10:00

Searched: 10:00-

Pred. No. is the number of results predicted by chance to have a

em_htgo_hum:* em_htgo_mus:* em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUPPORTES

Description	516 Seque	AX418525 Sequence	AX418595 Sequence	AR038979 Seguence	AR107371 Sequence	AR179333 Sequence	BEI 91596 Enzymatic	edrence	AD405888 Segmence	AD405892 Secrience	RD190590 Bioreacti	RD190635 Bioreact1	BD190639 Bioreact1	AR018981 Secuence	POLICIONAL SPECIAL	Something Sections	AD179335 Semience	AVAIGET GAMIANCA	PATER DESCRIPTION	777 TO 00 10 10 10 10 10 10 10 10 10 10 10 10	BULY1096 Bitymaric	Λι	AK405868 Sequence	ADADED BLOIGHTON	DOLOGE A DOCTOR	AVAIOED COMINGE	ANALOS OSCOLANA	option Constant	AXA18591 Sections	APC18981 Semience	ACCEPTED COCOCOC	Anistra Segment	Section B		AR038993 Seguence	AR179347 Sequence	BD191610 Engymatic	AX418538 Sequence	AX777164 Sequence	AX777194 Sequence	AX777234 Sequence	O)	g)	S)	4		2005-WITE-81 BAD 25021	near FAI						(SO) SIONITI AO	
CI	AX418516	AX418525	AX418595	PB038979	LCETOLDA	25,502,04	2010100	50101010	00000101	AK	AK403832	060000000000000000000000000000000000000	0000000	AD010001	100000 TE	AK107373	AK10/3/5	AK1/9335	AX418518	AX418527	BD191598	AR107385	AR405868	BD190615	AK4 0586 /	BD190614	AX418520	AX418526	AX418597	***************************************	AKU38983	AR179337	BULYIOU	AK405883	O COORTOOK	789714	BD191610	AX418538	AX777164	AX777194	AX777234	AR107364	AR107369	AR107374	AX080704	ALIGNMENTS		20 bp DNA from Patent W00200006.	70 10	1011			blosensor for ions	A 2 03-JAN-2002;	
Query Match Length DB	100.0 20	100.0	100.0	0,00	0.00	0.00	0.001	0.001	0.001	100.0	100.0	0.001	100.0	0.001	100.0	100.0	100.0	100.0	100.0	100.0	100.0 43	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.0	95.0 43	95.0	95.0	95.0	0.56	201	93.0	0.00	92.0	4 92 0 48	4 92.0	61 0.06	0.09 8	91 0 06 8	8 90.0 103 6			•		X418516.1 G1:Z1523361	synthetic construct		u,Y. and bl.d. Jucieto acid enzyme	Patent: MO 0200006-A 2 03-JAN-2002;	THE BURKE OF TRUE
Result No. Score	000		30	٠,	• •		0 1																									31 18						-	1 -		9 5	3	•	٠.	. . .		T 1 516	2	ž	VERSION		REFERENCE 1		¥.	•

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PAT 20-APR-2002
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                                Gape
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Unclassfiled.
Unclassfiled.
1 (bases 1 to 30)
1 (bases 1 to 30)
1 (bases 2 to 30)
Enrymatic DNA unclecules that contain modified nucleotides Farsymatic DNA unclecules that contain modified nucleotides Fatent: US 6110462-A 9 29-AUG-2000,
Incation/Qualifiers
1 . organism="unknown"
/nol_type="unassigned DNA"
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Query Match
Best Local Similarity 100.0%; Pred. No. 23,
Matches 20, Conservative 0, Mismatches 0, Indels
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100.0%; Score 20, DB 6;
Best Local Similarity 100.0%; Pred. No. 22,
Matches 20, Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                               1 (bases 1 to 30)
Joyce, G.P. and Breaker, R.E.
Enrymatic DNA molecules
Patent: US 5807718-A 9 15-SEP-1998;
Location/Qualifiers
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    .30
    /organism="unknown"
    /mol_type="unassigned DNA"

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Sequence 9 from patent US 5807718.
AR018979
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Best Local Similarity 100.
Matches 20, Conservative
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AR179333/c
LOCUS
DEFINITION
ACCESSION
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VZRSION
KEYMORDS
SOURCE
ORGANISM
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AR107371/c
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JOURNAL
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AUTHORS
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AR038979/c
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TITLE
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/organisms synthetic construct*

/organisms synthetic Construct*

/orb xref="taxon:32630"

/orb xref="taxon:32630"

/orbe=rbescription of Combined DNA/RNA Molecule: Chimeric substrate"
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                 1.20
/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:33530"
/note="bescription of Combined DNA/RNA Molecule: Chimeric substrate"
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Nucleic acid enryme biosensor for ions
Nucleic acid enryme biosensor for ions
Patent: WO 0200006-A 81 03-JAN-2002;
THE BOAN OF TRUSTES OF THE UNIVERSITY OF ILLINOIS (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid enzyme biosensor for ions
Patent: WO 0200006-A 11 03-0AN-2002;
THE BOARD OF TRUSTESS OF THE UNIVERSITY OF ILLINOIS [US)
LOCALION/Qualifiers
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100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred: No. 23;
Matches 20; Conservative 0; Mismatches 9; Indels
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100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="texon:32630"
/noTe="Rh-17DDS"
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Sequence 81 from Patent W00200006.
AX*18595
                                                                                                                                                                                                                                                                                                           20 bp
Sequence 11 from Patent WO0200066.
AX418525
AX418525.1 GI:21523390
 Location/Qualifiers
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AX418595
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100.0%; Score 20; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      linear
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Unclassified.

E J (baces 1 to 38)

B T (baces 1 to 38)

Bioreactive allosteric polymucleotides

Bioreactive allosteric polymucleotides

AL Patent: U8 6630306-A 53 b7-ccr-2003;

Location/Oualifiers
Unclassified.

1 (Dases 1 to 38)
Breaker,R.R. allosteric polynucleotides
Bloreactive allosteric polynucleotides
Patent: U8 650206-A 8 07-0CT-2003,
Location/Oualifiere
1. .38
/organiem="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                      AR405888 3 from paterit U3 6630306.
Sequence 53 from paterit U3 6630306.
AR405888.1 GI:40154907
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Brasker, R.R.
Bioreactive allosteric polynucleotides
Patent: U8 6630306-A 57 07-0CT-2003;
Location/Qualifiers
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Sequence 57 from patent US 6630306.
RR405892
AR405893.1 GI:40154911
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Upage 1, and Breaker, R. R.
Ruxymatic DRA molecules
Ruxymatic DRA molecules
Pagent: JP 2002514080-A 9 14-KAY-2002;
PR 20-APR-1998 1998547359
PR 29-APR-1997 US 60/04528
PC 1240. PP 000768, ROMALD R BREAKER
PC C1201/68, C12A9/22, C07121/04
PC Strandedness: Single;
PC Topology: Linear;
FH Key
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1 (bases 1 to 30)

1 yore, G.P. and Braker, R.R.

Enzymatic DNA molecules

Patent: US 6326174-A 9 04-DEC-2001;

Location/Qualifiers

    .30
    /organism="unkmown"
    /mol_type="unassigned DNA"

    .30
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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BD191596 GT:33001335
JP 200254080-A/9.
unidentified
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      AR179333.1 GI:20220888
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae.
1 (bases, 1 to 38)
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PD 21-MAY-2002;
PP 18-DEC-1997 JP 1998528049
PR 19-DEC-1996 US 60/033684,08-AUG-1997 US EP CLEATS/09,CLZQL/68,CL7N1'
CC Strandedness: Single:
CC Topology: I:-
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100.0%; Score 20; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                         DB 6, Length 38;
21;
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Unclassified.

1 (bases 1 to 43)

1 (bases 1 to 43)

2 (ovce, G.F. and Breaker, R.R.

2 Barymatic DNA molecules

2 Barymatic Location/Qualifiers

1.05 8007118-A 11 15-8EP-1998;

2 Location/Qualifiers

43 ""nknown"
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Bioreactive allosteric polynucleotide.
BD190639.
BD190639.1 GI:33000378
JP 2002514913-A/57.
Rattue
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                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 21, Matches 20; Conservative 0; Mismatches
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1 (Dases 1 to 38)
Braker, R.R.
Braker, R.R.
Bloreactive allosteric polynucleotide
Patent: UP 2002514913-A 53 21-MAY-2002;
MN UP 2002514913-A/53
                                                                                                 PAT 17-JUL-2003
                                                                                                                                                                                  Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Butelaostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 [bases 1 to 38]
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PD 21-MAY-2002
PP 18-DEC-1897 JP 1998528049
PR 19-DEC-1897 US 60/033684,08-AUG-1897 US RONNLD R BRAKER
PC CLANIS/09,CI2MI/00,CI2Q1/68,CI2MI*'-'-
CC Strandedness: Single:
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Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels
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Location/Qualifiers
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                                                                                                38 bp DMA Bioreactive allosteric polynucleotide. BD190590
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                   BD190590.1 GI:33000329
JP 2002514913-A/8.
Rattus
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Nucleic acid enryme biosensor for ions
Patent: WO 0200006-A 4 03-JAN-2002;
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Location/Qualifiers
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Nucleic acid ensyme biosensor for lons

Racent: WO 020006-A 13 03-DAN-2002;

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                                               # Unknown.
Unclassified.
3 | (bases 1 to 43)
3 | (bases 1 to 43)
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AL Patent: US 6326174-A 11 04-DEC-2001;
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8equence 13 from Patent W00200006.
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synthetic construct
artificial sequences.
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Unclassified.
1 (basse 1 to 43)
1 (basse 2 to 43)
Barbas, C.F., Joyce, G., Santoro, S.W. and Kandasamy, S.
Barpastic DNA molecules that contain modified nucleotides
Farent: US 6110462-A 13 29-AUG-2000,
Location/Qualifiers
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Barbast(C.F., Joyce,G., Santoro,S.W. and Kandassmy,S.

Rarymatic DNA molecules that contain modified nucleotides

Rarymatic DNA molecules that contain modified nucleotides

Patent: US 6110462-A 11 29-AUG-2000;

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Matches 20; Conservative 0; Mismatches
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    .43
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                                                                                                                                                                                                 AR107373
Sequence 11 from patent US
AR107373
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AR107375
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Mammala; Butheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 (bases 1 to 69)
Braker R.R.
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                                     Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels
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Patent: JP 2002514913-A 33 21-MAY-2002;
ALE WIVERSITY
PL JE 200214913-A/33
PD 21-MAY-2002
PP 18-DRC-1997 UP 1998528049
PR 19-DRC-1997 US
PR 19-DRC-1996 US 60/033684,08-AUG-1997 US
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Strandedness: Single;
                                                                                                                                                                                                                                                                    Unknown.
Unknown.
Unclassified.
1 (base I to 69)
1 Breaker, R. R.
Bloreactive allosteric polynucleotides
Location/Qualifiers
Location/Qualifiers
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AR405868
AR405868.1 GI:40154887
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/organism="Rattus"
/mol_type="genomic DNA"
/db_xref="texon:10114"
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/organism="unknown"
/wol_type="genomic DNA"
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Key
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PP 18-DBC-1997
PR 19-DBC-1996
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BD190615
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AR405868
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Barbas, C.F., Joyce, G., Santoro, S.W. and Xandasamy, S.
Ensymatic DNA molecules that contain modified nucleotides
Patent: US 6110462-A 23 29-AUG-2000,
Location/Qualifiers
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100.0%; Score 2D; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels
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    1. .43
/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="texcm:32630"
/note="Zn-DNA"
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Sequence 23 from patent US 6110462.
AR107385
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/organism="unknown"
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BD191596
BD191596.1 GT:3300137
PZ 2002514080-A/11.
unidentified
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AR107385
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BD191598
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PAT 18-JUN-2002
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^organism="synthetic construct"

/organism=signed DNA"

/db_xref="taxon:28530"

/noTe="bescription of Combined DNA/RNA Molecule: Chimeric substrate"
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Nucleic acid enzyme biosensor for ions
Nucleic acid enzyme biosensor for ions
Patent: WO 0200006-A 12 03-JAN-2002;
TER BOARD OF TRUSTERS OF THE UNIVERSITY OF ILLINOIS (US)
LOCALLON/QUALIFIERS
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Nucleic acid enzyme biosensor for ions
Patent: WO 0200060-A 6 03-JAM-2002;

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Location/Qualifiers
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Matches 20; Conservative 0; Mismatches 0; Indels
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    .97
    forganism=synthetic construct*
    /mol_type="unassigned DNA"
    /db xref="taxon:35630"
    /noFe="DNA Template"

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Sequence 12 from Patent W00200006.
AX418526
AX418526.1 GI:21523391
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Sequence 6 from Patent W00200006.
AX418520
AX418520.1 GI:21523385
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                                   14 ACTCACTATAGGAAGAGATG 33
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ORGANISM
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AX418520/c
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AX418597
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Mammalia, Eutherla, Rodentia, Sciurognathi, Muridae, Murinae.
1 (bases 1 to 87)
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100.0%; Score 20; DB 6; Length 69; 100.0%; Pred. No. 20; ive 0; Mismatches 0; Indels
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Patent: JP 2002514913-A 32 21-MAY-2002;
ALUS UNIVERSITY
PN JP 2002514913-A/32
PD 21-MAY-2009
PP 18-DEC-1997 JP 1998528049
PR 19-DEC-1997 US 60/033684,08-MUG-1997 US
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Strandedness: Single;
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M Unknown.
Unclassified.

8 1 (bases 1 to 87)

8 Breaker,R.R.

Bloreactive allosteric polynucleotides

9b. Patent: US 6630306-A 32 07-OcT-2003;

1 coetion/Qualifiers

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BD190614
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AR405867 G191640154886
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/organism="Rattus"
/mol_type="genomic DNA"
/db_xref="taxon:10114"
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JP 2002514913-A/32.
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       Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conserva
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BD190614
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AR405867
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Joyce, G.F. and Breaker, R.R.
Engwatte DNA molecules
Parent: JP 2002514080-A 13 14-MAY-2002,
THB SCRIPPE RESERRCH INSTITUTE
PN JP 2002514080-A/13
PD 14-MAY-2002
PP 29-APR-1999 US 60/045228
PR 29-APR-1997 US 60/045228
PR 29-APR-1997 US 60/045228
PR 29-APR-1997 US 60/045228
CC 1201/68, C12N9/22, COTHZ1/04
CC Standedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Jenndard name= 'adenosineribonuc:cotide'
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95.04; Score 19; DB 6;
Best Local Similarity 95.04; Pred. No. 69;
Matches 19; Conservative 0; Mismatches
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Unclassified.

1 (bases 1 to 43)
Joyce,G.F. and Breaker,R.R.
Enzymatic DNA molecules
Patent: US 5807718-A 13 15-SEP-1998,
Location/Qualifiers
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Joyce, G.F. and Breaker, R.R.
Bnzymatic DNA molecules
Patent: US 6326174-A 13 04-DEC-2001,
Location/Qualifiers
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Sequence 13 from patent US 6326174.
AR179337

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/organism="unknown"
/mol_type="unassigned DNA"

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/mol_type="unassigned DNA"
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BD191600
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JP 2002514080-A/13.
unidentified
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BD191600
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//organism="synthetic construct"
//organism="synthetic DNA"
//mol_type="unassigned DNA"
//mole="taxon:32630"
//mole="bestription of Combined DNA/RNA Molecule: Chimeric substrate"
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Patent: WO 0200064-A 9 03-JAN-2002;
THE BOAR OF TRUSTESS OF THE UNIVERSITY OF ILLINOIS (US)
Location/Qualifiers
                                                                                                                                           Lu, Y. and Li, J.
Nucleic acid enzyme bicsensor for ions
Patent: WO 0200006-A 83 03-JAN-2002;
THE BOARD OF TRUSTES OF THE UNIVERSITY OF ILLINOIS (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon.32630"
/note="predicted secondary structure of the deoxyriboryme"
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100.0%; Score 20; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels
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      DNA
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   AX418597 107 bp
Sequence 83 from Patent W00200006.
AX418597 GI:21523462
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Matches 19; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 95.0%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                   ch 95.0%; Score 19; DB 6; Length 65; 18 similarity 95.0%; Pred. No. 66; 19; Conservative 0; Mismatches 1; Indele
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Joyce, G. F. and Breaker, R.R.
Enzymatic DNA molecules
Patent: US 5807718-A 23 15-SEP-1998;
Location/Qualifiers
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Joyce, G.F. and Breaker, R.R.
Brzywatic DNA molecules
Patent: US 6326.74-A 23 04-DEC-2001;
Location/Qualifiers
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Sequence 23 from patent US 5807718.
AR038993 AR038993.1 GI:5958356
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AR279347 1 1:20220902
AR179347.1 GI:20220902
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    107
    organism="unknown"
    /mol_type="unassigned DNA"

1. .65
/organism="Rattus"
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/do_xref="taxon:10114"
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Unclassified.
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AR179347
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae.
1. (bases 1 to 65)
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Best Local Similarity 95.04; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 95.0%; Pred. No. 66;
Matches 19; Conservative 0; Mismatches 1; Indels
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Bioreactive allosteric polymuclectide
Bioreactive allosteric polymuclectide
ALB UNIVERSITY
BY 2002514913-A/48
BY 2002514913-A/48
BY 12 2002514913-A/48
PY 18-DEC-1997 UP 1998528049
RONALD R BRAKER
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Strandedness: Single;

Topology: Litear;

N is an RNA A Linkage

Key

Location/Qualifiers.
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Unclassified.
Unclassified.
I (bases I to 65)
S Breakr, R.R.
Biorescrive allosteric polynucleotides
AL Parent: US 6630306-A 48 07-0CT-2003;
S Location/Qualifiers
Jurce /organism="unknown"
/mol_type="genomic DNA"
Location/Qualifiers.
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Sequence 48 from patent US 6630306.
AR405883

    .43
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JP 2002514913-A/48.
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AR405883
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PAT 14-JUL-2003

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92.0%; Score 18.4; DB 6; Length 48; 95.0%; Pred. No. 1.46*02; tive 0; Mismatches 1; Indels
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Patent: WO 03040301-A 18 15-MAY-2003,
Cyclacel Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                               1. .48
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/db_xref="taxon:32630"
/noTe="Primer"
                                              AX777164 48 bp 1
Sequence 18 from Patent WO03040301.
AX777164
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Sequence 48 from Patent WO03040301.
AX777194.1 GI:32694342
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Job time : 591.311 8ecs
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Nucleic acid enzyme biosensor for ions

Patent: WO 0200006-A 24 03-JAN-2002;

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/6candard name* 'adenosineribonucleotide'
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/organism=synthetic construct*/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="co-DNA"
                                                                                                                                                  1 (bases 1 to 107)
Oyoce, G.P. and Breaker, R.R.
Enzymatic DNA molecules
Patent: JP 2002514080-A.23 14-MAY-2002;
THE SCRIPPS RASRARCH INSTITUTE
PN JP 2002514080-A/23
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29-ARR-1998 JP 1998547359
29-ARR-1997 US 60/04528
GERALD P JOYGE, RONALD R BREANCER
C12Q1/68,C12N9/22,C07H21/04
Strandedness: Single;
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Sequence 24 from Patent WO0200006.
AX418538
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                                107 bp
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                                          Enzymatic DNA molecules.
BD191610.1 G1:33001349
JP 2002514080-A/23.
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                                                                                                                                                                                                                                                                                           Query Match 92.0%; Score 18.4; DB 6; Length 48; Best Local Similarity 95.0%; Pred. No. 1.4e+02; Matches 19; Conservative 0; Mismatches 1; Indels
Deak, P., Frenz, L., Glover, D. and Midgley, C. Cell cycle progression proteins
Patent: WO 030401301-A 48 15-MAY-2003;
Cyclacel Limited (GB)
Location/Qualifiers
                                                                                                                            1. .48
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon;32630"
/noTe="Primer"
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us-10-144-679-2.rng

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Ceptright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2004, 07:43:51; Search time 123.019 Seconds (without alignments) 690.658 Million cell updates/sec Title:

DS-10-144-679-2
Sequence: 1 actcactataggasagatg 20
Scoring table: IDENTITY_NUC Gapext 1.0
Scoring table: 1373863 Seqs, 2124059041 residues
Total number of hits satisfying chosen parameters: 6747726
Minimum DB Seq length: 0
Maximum DB Seq length: 2000000000
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Post-processing: Minimum Match 04

Maximum Match 1008
Listing first 45 summaries
Listing first 45 summaries

N Geneseq 29Jan04:*
1: geneseq 29Jan04:*
2: geneseq 29Jan06:*
3: geneseq 20Jan06:*
4: geneseq 20Jan06:*
5: geneseq 20Jan06:*
6: geneseq 20Jan06:*
7: geneseq 20Jan06:*
8: geneseq 20Jan06:*
9: geneseq 20Jan06:*
10: geneseq 20Jan06:*

Pred. No. is the number of results predicted by chancs to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

t o	Zn (II) -de	RNA-cleav	Brzymatic	Template	Template	Template	PCR prime	Primer 2	PCR prime	PCR exten	Substrate	Enzymatic	Enzymatic	Primer ol	Substrate	Ion-depen	Zinc-depe	Self-clea	Self-clea	RNA-cleav	Ion-depen	Single st	Enzymatic
Description	Aa145381	Aa145460	Aav82930	Asa \$2230	Abk10823	Abk10807	Aav36574	Aav36578	Aav36529	Aav69804	Aat34973	Aav82934	Aav82932	Aaa92232	A8892234	Aa145383	Aa145391	Aav36554	Aav36553	Aa145390	Aa145385	Aac34901	Aav82944
e	AL45381	PAL45460	AAV82930	AAA92230	ABK10823	ABX10807	AAV36574	AAV36578	AAV36529	AAV69804	AT34973	AAV82934	AAV82932	AAA92232	AAA92234	AL 45383	RAL45391	AAV36554	AAV36553	ALE5390	AL45385	MT34901	AAV82944
	9	9	~	Ē	7 9	9	7 7	~	7	7	7	7 7	~	~	~	7 9	9	7	7	9	7 9	7	7
Length DB	50	20	30	30	33	33	38	38	38	38	43	43	43	43	E	43	43	69	87	93	97	101	101
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.c	100.0	100.0	100.C	100.C	100.c	100.0
Score	20	20	20	50	20	50	20	ŝ	ş	2	50	20	50	20	50	50	20	20	20	20	20	20	20
Result No.	-4	7	G G	4	ທ	φ υ	7	∞	Φ	20	11	17	. 13	14	15	16	17	18	19	20	c 21	22	23

Synthetic G3 deoxyr Self-capp	Bell-phos RNA-cleav Ccbalf-clea Ccbalf-clea Enzymatic Primer ol Terminati	Probe #13 Probe #3. Probe #5. Probe #15 Probe #9.	Escherich Primer fo T7 promot Promoter T7 promot
Aaa92244 Aa145461 Abki 0821	ADALOS DE SE	Aat60641 Aat60581 Aat60581 Aat60590 Aat60596	Aac88919 Aax28399 Aaf76370 Aad27673 Aaf76369
AAA92244 AAL45461 ABK10821	AALUG2 AALGE8 AALGE69 AALGE02 AAAC2228 AAAS2233 AAAS2233	AAP60641 AAF60585 AAF60590 AAF60596	AAC88919 AAX28399 AAP76370 AAD27673
m 40 40	- m m m m o m n o	។ ហេ ហ ហ ហ ហ ។	40404
107	25 60 60 60 60 60 60 60 60 60 60 60 60 60	111111111111111111111111111111111111111	4 % 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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4 8 8 6 4 8 9 6	, 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	20000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4444 112444 112444

ALIGNMENTS

RESULT	LT 1
NA NA NA	AAL45381 ID AAL45381 standard; DNA; 20 BP.
ăЯ	AAL45381;
#E	06-JUN-2002 (first entry)
ă X	Zn(II)-dependent trans-cleaving deoxyribozyme 17E.
ž č č	Biogensor, ion detection, lead, zinc, cobalt, nucleic acid enzyme, mencaphar, fluorophora, sharodatarion, ion concentration, riborms, sa
¥8	
ă E E	Key Location/Qualifiers
2222	/*tag= /bound_n /note= AAL45380
eeeee	<pre>/*tag= b /*tag= c /*tag= c /*bound moiety= "xibozyme 17E" //note="binds nucleotides 1-9 of ribozyme 17B shown in All45380"</pre>
ž ž	W0200200006-A2.
a e i	03-JAN-2002.
X #	27-JUN-2001; 2001MO-US020557,
ZE:	27-JUN-2000; 2000US-00605558.
4 5 5	(UNII) CHIV ILLINOIS POUND.
12	Lu Y, 113 J?
18	WPL; 2002-130823/17.
555	New nucleic acid enryme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and
F	for determining the concentration of a particular ion in a solution.

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                                                enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photoderector. The biosemsors are useful for the sensitive and snelective detection of ions. The biosemsors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosemsors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribosyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                   present invention relates to biosensors, comprising a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/bound_mojety= "RWA-cleaving deoxyribozyme"
/note= "binds nucleotides 33-25 of the deoxyribozyme
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                                                                                                                                            Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme;
quencher; fluorophore; photodetector; ion concentration; zlbozyme;
                                                                                                                                                                                                         ö
                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  Sequence 20 BP; 8 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    RNA-cleaving deoxyribozyme substrate #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                               1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1, Fig 6; 57pp; English
            Claim 18; Fig 5; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-2000, 2000UB-0060555B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUN-2001; 2001WO-US020557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNII ) UNIV ILLINOIS FOUND.
                                                                                                                                                                                                                                                                                                                      AAL45460 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                          06-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200006-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          quencher; fluc
substrate; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lu Y, Li J;
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                                                                                                                                                                                                                                                                                                                                                AAL45460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_RNA
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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodeteror. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a substrate of a ribozyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is used in a method which involves the production of catalytic DNA molecules which can be used for cleaving targer nucleic acid molecules. Such DNA molecules can be used for cleaving targer nucleic medical such DNA molecules can be used in pharmaceutical and medical products (e.g. for wound debridement, clot dissolution), as well as in household items (e.g. derergents, dental hygiene products, meat tenderisers'). Other suitable substrates include those comprising or produced by picornaviruses, (e.g. HBV), gammaherpesvirinae (e.g. HBV), papticiomaviruses (e.g. HTV-1 and -1); [laviviruses, togaviruses, leukemia viruses (e.g. HTV-1 and -1); [laviviruses, contributing to immunodeficiency diseases and synchomes and retroviruses contributing to immunodeficiency diseases and synchomes and extra and eline immunodeficiency viruses and betalents viruses and feline immunodeficiency viruses and betalents viruses and solve in and feline immunodeficiency viruses and feline immunodeficiency viruses and feline immunodeficiency of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bnzyme, catalygis, cleavage, target, pharmaceutical, medical, substrate, regulator, detergent, dental hygiene, meat tenderiser; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New catalytic DNA molecules - having site-specific endonuclease activity in a substrate nucleic acid, used for cleaving target nucleic acid
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                               100.0%; Score 20; DB 6; Length 20; 100.0%; Pred. No. 3.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 30 BP; 5 A; 10 C; 6 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                             Sequence 20 BP, 8 A, 3 C, 5 G, 4 T, 0 U, 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 62, 161pp, English.
                                                                                                                                                                                                                                                                                                                  1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
AAV82930/c
ID AAV82930 standard, DNA; 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0045228P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US008677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzymatic DNA 30mer template.
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Joyce GP, Breaker RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-034670/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9849346-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV82930,
         8X8888888XX
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the present invention describes a catalytic twin molecule than expension throation describes a graph proposition to the catalytic DRA molecule comprises at least one pyrimidine included the catalytic DRA molecule, capable of hydrolytic cleavage of a nucleic acid phosphosefer bond. The catalytic DNA molecule capable of hydrolytic cleavage of a nucleic acid phosphosefer bond. The catalytic DNA molecule of a negal extranded nucleic acid in the absence. This is useful for cleavage of a nucleic acid phosphosefer bond. This is useful for cleavage containing and genetic empirication. This is useful in methods of engine at a specific position. This is useful in methods of engine is composed of only 12 residues, making this one of the amallest nucleic acid catalysts known. The catalytic core of the anallest nucleic acid catalysts known. The catalytic core of the anallest nucleic acid catalysts known. The catalytic core of the smallest nucleic acid catalysts known. The catalytic core of the smallest nucleic acid catalysts the 3 imidazole-containing residues. The enzyme can be made to cleave RNA of almost any sequence by simple alteration of the concentrations of 2024, exhibiting seturation kinetics and a catalytic core concentrations of 2024, exhibiting seturation kinetics and a catalytic core substrate-recognition properties of nucleic acid enzymes and the chemical functionality of protein enzymes in a molecule that is small in size, yet of present invention engalesing in the exemplification of the core. The present invention of the core of the catalytically efficient. The present sequence represents an olicy the catalytic core of the core of the catalytically efficient. The present sequence represents and a catalytically efficient. The present sequence represents and catalytically efficient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Catalytic; enzymatic; modified nucleotide; enzymė, site-specific, target; substrate; template; primer; cleavage; hydrolytic cleavage; nucleic acid phosphoester bond; cloning; genetic engineering; ss.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensymatic DNA molecules containing modified nucleotides useful for cleavage of RNA at a specified position.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a catalytic DNA molecule that
100.0%; Score 20; DB 2; Length 30; 100.0%; Pred. No. 3.4; tve 0, Nismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30 BP; 5 A; 10 C; 6 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kandasamy S, Joyce G, Santoro SW;
                                                                                                                                                                                                                                                                                                                                                                                           Template oligonucleotide sequence SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Col 29; 52pp; English.
                                                                                              1 ACTCACTATAGGAAGAGATG 20
                                                                                                                               21 ACTCACTATAGGAAGAGATG Z
                                                                                                                                                                                                                                                    AAA92230 standard, DNA, 30 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00262142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00262142.
                                                                                                                                                                                                                                                                                                                                                  09-JAN-2001 (First entry)
     Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-593449/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6110462-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barbas CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                       AAA92230;
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/*tag* a //*tag* a //bound moiety= "Self-phosphorylating deoxyribozyme" //bound moiety= "Porms a double stranded region with bases 18-6 of the sequence in ABK10821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New conjoined polynucleotides comprising a kinase domain and an adenylase domain, useful in DNA cloning, for carrying out sequential polynucleotide manipulations in a serial fashion, or for polynucleotide manipulations.
                                                                                                                                                                                                                                              Self-capping decxyribosyme; conjoined polynuclectide; catalyst; ribozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a conjoined polynucleotide comprising at least two catalytic domains which function in concert to provide a chemical transformation involving multiple sequential reactions. The use of the conjoined polynucleotides as catalysts offer advantages over protein-based enzymes in cloning and in a number of commercial and industrial processes. Onlyined polynucleotides made from DNA are expected to be much more stable, and can be easily made by automated oligonucleotide synthesis, and DNA is significantly more resistant to hydrolytic degradation compared to RNA. Conjoined DNA and RNA may be selected for their activity when immobilised. This sequence represents a template strand used in the selection protocol for self-capping deoxyribozymes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Indels
                                                                                                                                                                                                             Template DNA for self-capping deoxyribozyme selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33 BP; 6 A; 8 C; 7 G; 12 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0, Mismatches
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 58; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACTCACTATAGGAAGAGATG 20
1 ACTCACTATAGGAAGAGATG 20
                             21 ACTCACTATAGGAAGATG 2
                                                                                                    1823/c
ABK10823 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-0CT-2000, 2000WO-US028508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9908-0159808P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            described in the invention
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-226120/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200129249-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-0CT-1999,
                                                                                                                                                                          21-KAY-2002
                                                                                                                                                                                                                                                                                                                                            misc binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breaker RR;
                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                             ABK1 0823;
                                                                                                RESULT
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25 ACTCACTATAGGAAGAGATG

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0; Gaps

Ouery Match 100.0%; Score 20; DB 3; Length 30; Best Local Similarity 100.0%; Pred. No. 3.4; Matches 20; Conservative 0; Mismatches 0; Indels

ABK10807;

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PCR primers ANV36574-75 were used in the course of the invention. The specification describes an allosteric DNA polynucleotide which can modify a function or configuration of the polynucleotide with a chemical effector and/or a physical signal. The allosteric polynucleotides can be used for detecting the presence or concentrations of compounds such as amino acids, peptides, nucleosides, nucleotides, steroids, microbial or cellular metabolites, blood or urine components, pharmaceuticals, pesticides, herbicides, or food toxins. The allosteric polynucleotides can also be used for detecting physical signals such as radiation and temperature changes. The polynucleotides can also be used in biosensors, in which they are more stable than proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allosteric polynucleotides - having modified function or configuration, used for the production of biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer 2 used to prepare the DNA pool and amplify deoxyribozymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allosteric DNA polynucleotide; modify, function, configuration, detection, biosensor, PCR primer; ss.
                                                                            Allosteric DNA polynucleotide; modify; function; configuration; detection; biosensor; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38 BP; 13 A; 9 C; 8 G; 8 T; 0 U; 0 Other;
                                     PCR primer used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3, Page 72, 106pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 ACTCACTATAGGAAGAGATG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV36578 standard; DNA; 38 BP.
                                                                                                                                                                                                                                                                                                               96US-0033684P.
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                                                                                                                                                                                                                                                                          97WO-US024158
09-CCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                             (UYYA ) UNIV YALE.
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                                                                                                                                                                                      MO9827104-A1
                                                                                                                                                                                                                                                                          8-DEC-1997;
                                                                                                                                                                                                                                                                                                                 19-DEC-1996;
08-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Breaker RR,
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV36578;
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/bound_moiety= "Self-phosphorylating deoxyribozyme"
/bound_moiety= "Forms a double stranded region with bases 38-6 of
the sequence in ABK10822*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New conjoined polynuclectides comprising a kinase domain and an adenylase domain, useful in DNA cloning, for carrying out sequential polynuclectide manipulations in a serial fashion, or for polynuclectide manipulations.
                                                                                                                                                                                                         Self-phosphorylating deoxyribosyme; conjoined polymucleotide; catalyst;
ribosyme; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a conjoined polynucleotide comprising at least two catalytic domains which function in concert to provide a chemical cransformation involving multiple sequential reactions. The use of the conjoined polynucleotides as catalysts offer advantages over protein-based enzymes in cloning and in a number of comercial and industrial purchases. Conjoined polynucleotides made from DNA are expected to be much more stable, and can be easily made by automated oligonucleotide synthesis, and DNA is significantly more resistent to hydrolytic their ability to function on solid support and are expected to retain their activity when immobilised. This sequence represents a template decoxyribozymes, described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                  Template DNA for self-phosphorylating deoxyriboryme selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 100.0%; Score 20; DB 6; Length 33; Local Similarity 100.0%; Pred. No. 3.4; les 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33 BP; 6 A; 9 C; 6 G; 12 T; 0 U; 0 Ochez;
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACTCACTATAGGAAGAGATG 20
  RESULT 6
ABK10807/c
ID ABK10807 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV36574 standard; DNA; 38 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-2000, 2000MO-US028508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0159808P
                                                                                                                             21-MAY-2002 (first entry)
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misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breaker RR;
                                                                                                                                                                                                                                                                              Synthetic.
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Query Match

ò 셤 AAV36574

RESULT 7
LAV36574
ID AAV3
XX
AX
AC AAV3

Gaps

Gaps

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PCR primers AAV36528-29 were used in the course of the invantion. The specification describes an allosteric DAA polymucleotide which can modify a function or configuration of the polymucleotide with a chemical effector and/or a physical signal. The allosteric polymucleotides can be used for detecting the presence or concentrations of compounds such as amino acids, peptides, nucleosides, nucleotides, seroids, microbial or cellular metabolites, blood or unine components, pharmaceuticals, pesticides, harbicides, or food toxins. The allosteric polymucleotides can also be used for detecting physical signals such as radiation and temperature changes. The polymucleotides can also be used in biosensors, in which they are more stable chan proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid with endonuclease activity - used to cleave targetted for modulating gene expression in plant or animal cells, particularly treatment or diagnosis of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity. The nucleic acids of the invention can cleave a target nucleic acid, particularly RNA, for modulation of gene expression in plant or animal cells, e.g. for disgnosis and/or treatment of diseases, such as inhibitation of cell proliferation, and also for examining genetic drift and mutations in cells rolls to detect the target (mutant or wild-type) in cells and possibly for RNA sequencing. The nucleic acids, optionally completed with cationic lipid, are delivered to smooth muscle calls (via catheter or stent, incorporated in hipplymer and by injection), or vectors that express them are introduced into cells ex vivo or in vivo. The nucleic scids catals endered acids catalyse both intra- and inter-molecular endonuclease reactions in a sequence-specific manner, and are not homologous with known ribosymes. They can be designed to target almost any RNA transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hammerhead ribozyme; nucleic acid catalyst; synthesis; target; ATP-dependent allosteric ribozyme; endoudlease activity; cleave; modulating gene expression; treatment; diagnosis; genetic drift; mutation; cell proliferation; PCR primer; se.
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0
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                                                                                                                                                                                                                                                                                                                    100.0%; Score 20; DB 2; Length 3B; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                          Sequence 38 BP; 14 A; 7 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 37; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
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                                                                                                                                                                                                                                                                                                                                                                                                                                              14 ACTCACTATAGGAAGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV69804 standard; DNA; 38 BP.
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                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV69804;
                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                               PCR primers AAV36576-78 were used to amplify the DNA pool, and selected sel-cleaving DNAs (decayribozymes). The specification describes an allosferic DNA polymorlectide which can modify a function or configuration of the polymorlectide with a chemical effector and/or a physical signal. The allosteric polymorlectides can be used for detecting the presence or concentrations of compounds such as amino acids, peptides, nucleosides, nucleotides, steroids, microbial or callular metabolites, blood or urine components, pharmaceuticials, pesticides, harbicides, or food coarins. The allosteric polymorlectides can also be used for detecting physical signals such as radiation and temperature changes. The polymorlectides can also be used in blosensors, in which
                                                                                                                                                                                                         Allosteric polymucleotides - having modified function or configuration, used for the production of biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allosteric polynucleorides - having modified function or configuration, used for the production of biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allosteric DNA polymucleotide; modify; function; configuration; detection; biosensor; PCR primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 2; Length 38; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38 BP; 14 A; 7 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer 2 used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                            Example 3; Page 47; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          they are more stable than proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Pig 9B; 106pp; English
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            9608-0033684P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity and see 201 Conservative
                                                                                                                                                                    WPI; 1998-362715/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-362715/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
rocal Similarity
                                                                          (UYYA ) DNIV YALE.
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              19-DEC-1996;
08-AUG-1997;
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                                                                                                                         Breaker RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breaker RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Matches
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and since they are relatively small are reasonably inexpensive to produce. The present sequence represents a PCR extension reaction primer used in an example from the present invention for in vitro selection
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                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substrate for ssDNA molecules having site-specific cleavage activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endonuclease; cleavage; RNA; catalyst; wound debzidement; clot dissolution; meat tenderiser; viral infection; dental hygiene; detergent; enzyme isolation; ss.
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/note= "adenosine ribonucleotide, cleavage site"
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Best Local Similarity 100.0%; Score 20; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43 BP, 15 A, 8 C, 12 G, 8 T; 0 U, 0 Other,
                                                                                                                                                    Sequence 38 BP; 14 A; 7 C; 9 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       1 ACTCACTATAGGAAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                  14 ACTCACTATAGGAAGAGATG 33
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95US-00472194.
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misc_feature
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A A 149.13
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This sequence is used in a method which involves the production of catalytic DNA molecules which can be used for cleaving target nucleic acid molecules. Such DNA molecules can be used in pharmaceutical and medical products (e.g. for wound destriement, clot dissolution), as well as in household items (e.g. detergents, dental hygiene products, meat renderisers). Other sultable substrates include those comprising or produced by picornaviruses, hepsdawiridae, (e.g. HBV, HCV), pspttiomaviruses (e.g. HPV), gammaharpesvirinae (e.g. HBV, HCV), pspttiomaviruses (e.g. HTV-1 and -11;, larghtviruses, togaviruses, between a viruses (e.g. HTLV-1 and -11;, all aviviruses), cytomegaolytiuses (including alphaberpesviruse and betaherpesviruses contributing to immunodeficiency diseases and syndromes and retroviruses contributing to immunodeficiency viruses and bovine jeukemia viruses. They can also be used as regulators of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New catalytic DNA molecules - having site-specific endonuclease activity in a substrate nucleic acid, used for cleaving target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rasyme, catalysis, cleavage, target, pharmaceutical; medical; substrate; regulator; detergent, dental hygiene; meat tenderieer; ss.
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/note= "ribonucleotide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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1 ACTCACTATAGGAAGAGATG
                                                       19 acreactaraccaacate
                                                                                                                                                                                                                             AAV82934 standard, DNA; 43 BP.
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                                                                                                                                              Ensyme; catalysis; cleavage; target; pharmaceutical; medical; substrate; regulator; detergent; dental hygiene; meat tenderiser; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                             New catalytic DNA molecules - having site-specific endonuclesse activity in a substrate nucleic acid, used for cleaving target nucleic acid
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                             AAV62932 standard, DNA, 43 BP.
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                                                                                                                                                                                                                                                                                                                                        (SCRI ) SCRIPPS RES INST.
                                                                                                                  Enzymatic DNA primer 2.
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                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-034670/03.
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                                                                                                                                                                                                                       WO9849346-A1.
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Best Local S:
Matches 20
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   RESULT 13
AAV82932
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The present invention describes a catalytic at a defined cleavage site, where the catalytic DNA molecule comprises at least one pyrimidine uncleared in (1) (1) is a catalytic DNA molecule, capable of hydrolytic cleavage of a mucleic acid phosphoester bond. The catalytic DNA molecule can assert the a mucleic acid in the molecule, capable of hydrolytic cleavage of a mucleic acid in the absence of a restriction of single-arranded mucleic acid in the absence of a restriction and muclease site a specific position. This is useful for cleavage of a single-arranded mucleic acid in the absence of a restriction of the mucleic acid only 12 residues, making this one of the simplination crayme is composed of only 12 residues, making this one of the malliest nucleic acid catalysic core forms a compact hairpin the margine the indiatole-containing residues. The enzyme can be made to cleave RNA of almost any sequence by simple alteration of the two substrate-recognition domains that surround the catalytic core. The carryme operates with multiple turnover in the presence of micromolar concentrations of Zn3+, exhibiting sequencion kinetics and a catalytic care uncatalysed reaction. The imidazole-containing DNA enzyme and the chemical substrate-recognition properties of nucleic acid enzymes and the chemical correction. The imidazole-containing DNA enzyme and the chemical correction into properties of nucleic acid enzymes and the chemical correction. The indiatole-containing DNA enzyme and the chemical correction into properties of nucleic acid enzymes and the chemical correction. The indiatole-containing DNA enzyme and the chemical correction into properties of nucleic acid enzymes and the chemical correction. The present sequence represents an engagement of properties of correction of the correction of the present sequence represents an engagement of approximately and engagement of a used in the exemplification of the correction.
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substrate, template, primer, cleavage, hydrolytic cleavage, nucleic acid phosphoester bond, cloning, genetic enginecting, as
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100.0%; Score 20; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels
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The present invention describes a catalytic DNA molecule that

specifically cleaves a substrate nucleic acid at a defined cleavege site,
where the catalytic DNA molecule comprises at least one pyrimidine
nucleotide (I). (I) is a catalytic DNA molecule, capable of hydrolytic
cleavage of a nucleic acid phosphoseter bond. The catalytic DNA molecule
is used to cleave NNA of almost any sequence. This is useful for cleavage
of single-stranded nucleic acid in the absence of a restriction
conductance site at a specific posttion. This is useful in methods of
c.g. cloning and genetic engineering. The catalytic core of the minimised
anyme is composed of only 12 residues, making this one of the single-
catalytic core for manipulation of the concurred and state anyme can
be ructure displaying the 3 imidatole-containing residues. The enayme can
be made to cleave RNA of almost any sequence by simple alteration of the
curyme operates with multiple turnover in the presence of micromolar
concentrations of zn2+, exhibiting saturation kinetics and a catalytic
concentrations of zn2+, exhibiting saturation kinetics and a catalytic
concentrations of zn2+, exhibiting saturation functions and a catalytic
curvatalysed reaction. The imidatole-containing DNA enzyme combines the
substrate-recognition properties of nucleic acid enzymes and the chemical
curvatalysed reaction. The imidatole-containing DNA enzyme combines
concentrationality of protein enzymes in a molecule that is small in size, yet
concentrations the sequence which is used in the exemplification of the
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                                                                                                                                                   /*tag= a
/note= "adenosine ribonucleotide"
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                                                                 Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                        9938-00262142
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                                                                         Key
modified_base
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Synthetic.
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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher ox/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of ar ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a PCR primer used to isolate a ribozyme which may be used as a biosensor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; ribozyme; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43 BP, 15 A, 9 C, 10 G, 9 T, 0 U, 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-dependent deoxyribozyme SEQ ID NO: 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL45391 standard, DNA; 43 BP.
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selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.

New mucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead io

WPI; 2002-130823/17.

Lu Y, Li J;

27-JUN-2001; 2001WO-U8020557. 27-JUN-2000; 20CQUS-00605558. (UNII) DNIV ILLINOIS FOUND.

W0200200006-A2

03-JAN-2002

Unidentified.

primer; se.

96US-0033684P.

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Allosteric polynucleotides - having modified function or configuration, used for the production of biosensors.
                                                                                                                                                                                                                  MPI; 1998-362715/31.
                                                                                                  (DYYA ) UNIV YALB
                     19-DEC-1996;
08-AUG-1997;
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                                                                                                                                                                                   The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quancher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
                                                       and
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                        New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, for determining the concentration of a particular ion in a solution.
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22. .41
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/note= "hybridises with nucleotides 13-18"
57 . 67
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57. 60
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/note= "hybridises with nucleotides 64-67"
64. 67
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Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels
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'note= "hybridises with nucleotides 22-25*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 ACTCACTATAGGAAGAGATG 38
                                                                                                                                           Example 1; Pig 2; 57pp; English.
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NX ANA 36534
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                                    The present sequence represents a self-cleaving DNA molecule of the invention. The specification describes an allosteric DNA polymucleotide which can modify a function or configuration of the polymucleotide with a comprise the present sequence. The allosteric polymucleotide can comprise the present sequence. The allosteric polymucleotides can be used for detecting the presence or concentrations of compounds such as amino acids, peptides, nucleosides, nucleotides, steroids, microbial or cellular metabolites, blood or urine components, pharmaceuticals, pesticides, harbicides, or food toxins. The allosteric polymucleotides can also be used for detecting physical signals such as radiation and temperature changes. The polymucleotides can also be used in biosensors, in which they are more stable than proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Self-cleaving DNA, allosteric DNA polymucleotide, modify, function, configuration, detection; biosensor; ss.
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/*tag= f
/*tag= f
/*tag= hybridises with nucleotides 64-65*
64. .65 /*tag= g
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/*tag= a
/note= "hybridises with nuclectides 83-37"
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/notes "hybridises with nucleotides 18-22"
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note= *hybridises with nucleotides 39-43*
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                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 69 BP; 21 A; 13 C; 16 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 3.6
Matches 20; Conservative 0; Mismatches
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Claim 6, Fig 14A, 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACTCACTATAGGAAGAGATG 20
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18. .22
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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biogensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; zibosyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 20; DB 6; Length 97;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 20; Conservative 0; Mismatches 0; Indels
                  /'tags a
/bound_moletys "nucleotides 82-79"
/notes "binds nucleotides 82-79 of itself"
                                                                                                                                         /*tag= c
/bound molety= "nucleotides 14-11"
/note= "binds nucleotides 14-11 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 97 BP; 17 A; 13 C; 15 G; 12 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jon-dependent deoxyribozyme random DNA pool template.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACTCACTATAGGAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 1; 57pp; English.
                                                                                                                                                                                                                                                                                                        27-JUN-2001; 2001WO-USD20557.
                                                                                                                                                                                                                                                                                                                                                27-JUN-2000; 2000US-00605558.
                                                                                                                                                                                                                                                                                                                                                                                     (UNII ) UNIV ILLINOIS FOUND.
                                                                            23. 38
/*tag= b
79. 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-130823/17.
                                                                                                                                                                                                                             WO200200006-A2.
misc_binding
                                                                                                                       misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                             tu Y, 14 J,
                                                                                                                                                                                                                                                                    03-JAN-2002.
                                                                                 stem_loop
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a self-cleaving DNA molecule of the invention. The specification describes an allosteric DNA polymucleotide which can modify a function or configuration of the polymucleotide with a chemical effector and/or a physical signal. This polymucleotide can comprise the present sequence. The allosteric polymucleotides can be used for detecting the presence or concentrations of compounds such as amino acids, peptides, nucleosides, nucleotides, steroids, microbial or callular metabolites, blood or urine components, pharmaceuticals, pesticides, broad or urine components, pharmaceuticals, pesticides to an also be used for detecting physical signals such as radiation and temperature changes. The polymucleotides can also be used in biosensors, in which they are more stable than proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allosteric polynucleotides - having modified function or configuration, used for the production of biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; zibozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                   /notes "hybridises with nucleotides 75-81"
75. 81 /*tsgs j
/notes "hybridises with nucleotides 65-72"
83. 87 /*tsgs k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 20; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels
         /note= "hybridises with nucleotides 51-52"
                                                                                                                                                                                                                             /note= "hybridises with nucleotides 4-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 87 BP; 28 A; 14 C; 26 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Fig 12B; 106pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-cleaving deoxyribozyme #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAL45390 standard; DNA; 97 BP.
                                                                                                                                                                                                                                                                                                                                                     97WO-US024158
                                                                                                                                                                                                                                                                                                                                                                                           96US-0033684P
97US-0055039P
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                                             Д.
                                               *tag=
                                                                                          *tag=
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                                                                        misc_structure
                                                                                                                                                                                           misc_structure
                                                                                                                                misc_structure
                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996;
08-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                     18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                        WO9827104-A1
                                                                                                                                                                                                                                                                                                               25-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breaker RR;
                                 stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL45390,
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AMI45390
LID AMI45390
LID AMI45390
LID AMI45
AMI

8 용 Key

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Gaps ô õ

Gaps ö

0, Indels

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This sequence is used in a method which involves the production of catalytic DNA molecules which can be used for cleaving target nucleic actalytic DNA molecules which can be used for cleaving target nucleic medical products (e.g. for wound debridement, clot dissolution), as well as in household teems (e.g. detergents, dental hygiene products, meat tenderisers'). Other suitable substrates include those comprising or produced by picornaviruses, hepadnaviridae, (e.g. HBV, HCV), pammaharpevirinae (e.g. HBV, HCV), pammaharpevirinae (e.g. EBV; lymphocryptoviruses), leukenia viruses (e.g. HELV-1 and -11); tlavitviruses, togaviruses, herpesviruses (ficcluding alphaherpesviruse and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New catalytic DNA molecules - having site-specific endonuclease activity
in a substrate nucleic acid, used for cleaving target nucleic acid
sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensyme, catalysis, cleavage, target, pharmaceutical; medical; substrate; regulator, detergent, dental hygiene, meat tenderiser; ss.
      AMINABIL-T14967 are single stranded (ss), non-naturally occurring DNA molecules that have site-specific endonuclesse activity. The carelytic DNA molecules specifically cleave so nucleic acids, esp. RNA sequences. The carelytic DNAs may be used in medicine e.g. for wound debridement, cloc dissolution, etc., or in detergence, dental hygiene products and meat tenderisers. The DNAs may be useful to treat viral infections such as HIV when targetted to viral nucleic acid and they may be expressed in a target host cell. In vira selection of the DNAs allows the isolation of catalysts/ensymas without the need for prior knowledge of their compen. or structure
                                                                                                                                                                                                                                                                                 Score 20, DB 2; Length 107;
Pred. No. 3.7;
                                                                                                                                                                                                                                          Sequence 107 BP, 20 A; 14 C; 19 G; 14 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "ribonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 70, 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                    38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAVB2944 standard; DNA; 107 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic DNA 107mer oligomer.
                                                                                                                                                                                                                                                                                                                                                                                                    19 ACTCACTATAGGAAGAGATG
                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity 100.07
Warches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Joyce GF, Breaker RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI, 1999-034670/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV82944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV82944
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                                                                                                                                                                                                                                                          The present invention relates to biosensors, comprising a nucleic acid enryme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a sequence described in the exemplification of the invention
                                                                                                                                     New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA with site specific endonuclesse activity - partic. for cleavage of RNA, e.g. for medical use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endonuclease, cleavage; RNA, catalyst; wound debzidement;
clot dissolution, meat tendeziser; viral infection, dental hygiene;
detergent; enzyme isolation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single stranded DNA with site specific endonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 6; Length 97; 100.0%; Pred. No. 3.6; ive 0; Miscatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 97 BP; 12 A; 16 C; 12 G; 17 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag* a
/note= "adenosine ribonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 66; 114pp; English.
                                                                                                                                                                                                                            Example 1, Page 23, 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 ACTCACTATAGGAAGAGATG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT34901 Standard; DNA; 107 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACTCACTATAGGAAGATG
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                         (UNII ) UNIA ITTINOIS BOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-286834/29.
                                                                                                         WPI; 2002-130823/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1995;
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                                                                Lu Y, Li J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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misc_binding
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                                                                                                                                                                                                                                                    The present invention describes a catalytic DNA molecula that specifically cleaves a substrate mucleic acid at a defined cleavage site, where the catalytic DNA molecule comprises at least one pyrimidine nucleotide [1]. [1] is a catalytic DNA molecule, capable of hydrolytic cleavage of a nucleic acid phosphoester bond. The catalytic DNA molecule of elastic cleavage of a nucleic acid in the absence of a restriction of single-stranded nucleic acid in the absence of a restriction of elasgies atte at a specific position. This is useful for cleavage of of cleavage of an ordinary and genetic enginearing. The catalytic core of the minimised enzyme is composed of only 12 residues, making this one of the smallest nucleic acid catalytes known. The catalytic core of the minimised enzyme is composed of only 12 residues, making this one of the smallest nucleic acid catalytes core force of the minimised enzyme is composed of almost any sequence by simple alteration of the two substrate-recognition domains that surround the catalytic core. The consyme operates with multiple turnover in the presence of micromolar concentrations of $274+, exhibiting saturation kinetics and a catalytic create enhancement of approximately 1000000-fold compared to the substrate-recognition properties of nucleic acid earlytic such the substrate-recognition properties of nucleic acid earlytic such the functionality of protein ensymes in a molecule that is small in size, yet versatile and cetalytically efficient. The present sequence represents an
                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                              Catalytic; enzymatic; modified nucleotide; enzyme; site-specific; target; substrate; template; primer; cleavage; hydrolytic cleavage; nucleic acid phosphoester bond; cloning; genetic engineering; ss.
betaherpesviruses), cytomegaolviruses (CMV), influenta viruses, viruses and retroviruses contributing to immunodeficiancy diseases and syndromes (e.g. Hiv-1 and -2), sinian and feliane immunodeficiency viruses and bovine leukemia viruses. They can also be used as regulators of gene
                                                                                                                                                Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzymatic DNA molecules containing modified nucleotides useful for cleavage of RNA at a specified position.
                                                                                                                                                ö
                                                                                                            ; Score 20; DB 2; Length 107;
; Pred. No. 3.7;
0; Mismatches 0; Indels
                                                                                    Sequence 107 BP; 20 A; 14 C; 19 G; 14 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Joyce G, Santoro SW;
                                                                                                                                                                                                                                                                                                                                                                    Synthetic oligomer sequence SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4, Col 33, 52pp, English.
                                                                                                                                                                           1 ACTCACTATAGGAAGATG 20
                                                                                                                                                                                               19 ACTCACTATAGGAAGATG 38
                                                                                                                                                                                                                                                                                AAA92244 Btandard; DNA; 107 BP.
                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00262142.
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                                                                                                                                                                                                                                                                                                                                       09-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barbas CF, Kandasamy S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-593449/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6110462-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2000.
                                                               expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                    RESULT 24
AAA92244
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      88888888
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the
                                                                                                                                  Gape
oligonucleotide sequence which is used in the exemplification of
                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'bound modety= "nucleotides 108-107"
'note=""binds nucleotides 108-107 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bound moiety= "nucleotides 102-101"
note= "binds nucleotides 102-101 of itself"
                                                                                       ; Score 20; DB 3; Length 107; Pred. No. 3.7; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= e
bound_moiety= "nucleotides 69-67"
'note= "binds nucleotides 69-67 of itself"
                                                       Sequence 107 BP; 20 A; 14 C; 19 G; 14 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= b
bound_moiety= "nucleotide 105"
'note= "binds nucleotide 105 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'bound moiety= *nuclectide 104"
'note= "binds nucleotide 104 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= 1
/bound_moiety= "nucleotide 22"
/note= "binds nucleotide 22 of itself"
67. 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*rag= g
/bound_molety= "nucleotide 64"
/note= "binds nucleotide 64 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= k
/bound_moiety= "nucleotide 24"
/note= "binds nucleotide 24 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *cag= f
bound_moiety= "nucleotide 66"
note= "binds nucleotide 66 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                       1 ACTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                 19 ACTCACTATACGAAGAGATG 38
                                                                                                                                                                                                                                                                                                          AAL45461 standard, DNA; 107 BP.
                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 20, Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.50
/*tag= i
/*tag= j
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                         G3 deaxyribozyme.
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The invention describes a conjoined polynucleotide comprising at least two catalytic domains which function in concert to provide a chemical transformation involving multiple sequential reactions. The use of the conjoined polynucleotides actaalysts offer advantages over proteinbased enzymes in cloning and in a number of commercial and industrial processes. Conjoined polynucleotides made from DNA are expected to be much more stable, and can be easily made automated oligonucleotide symbosis, and DNA is significantly more resistant to hydrolytic degradation compared to RNA. Conjoined DNA and RNA may be selected for their activity when immobilised. This sequence represents an acceptor construct used in the selection of self-capping deoxyribozymes, described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New conjoined polynucleotides comprising a kinase domain and an aderylase domain, useful in DNA cloning, for carrying out sequential polynucleotide canipulations in a serial fashion, or for polynucleotide manipulations.
                                                                                                          //trag= a
/bound_moiety= *ABK10823*
/bound_moiety= *ABK10823*
strand_shown_in_ABK10823*
                                                                                                                                                                                                                                                                                                                     /*tag= d
/bond_moiety= "primer 1"
//note= "The sequence for primer 1 is not given in the
specification"
                                                                                                                                                                                    23. .24 , ^{\prime}*eag= ^{\prime} b ^{\prime} hore= ^{\prime} capping and ligation site of deoxyribozyme=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 123; Score 2C; DB 6; Length 123; Similarity 100.0%; Pred. No. 3.7; 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  39. .108
/*tag= c /note= "Random sequence of 70 nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 123 BP; 17 A; 10 C; 14 G; 12 T; 0 U; 70 Other;
ribozyme; self-capping deoxyribozyme; ss.
                                                      Location/Qualifiers
6. 38
7.tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sxample 1, Fig 5B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABKL0822 standard; DNA; 123 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0159808P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-0CT-2000; 2000WD-US028508
                                                                                                                                                                                                                                                                                                .123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPI, 2002-226120/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In the invention
                                                                                                                                                                                                                                                                                                                                                                                                             W0200129249-A2
                                                                      Key
misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-0CT-1999,
                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-2001
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                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABKL 0822 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ABK10622
1D ABK10
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AC ABK10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to blosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a ribozyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Self-phosphorylating deoxyribozyme; conjoined polynucleotide; catalyst;
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Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 20, Conservative D; Mismacches O; Indels
      /*tag* m
/bound_moiety= "nucleotides 18-16"
/note= "binds nucleotides 18-16 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salf-capping deoxyribozyme selection, acceptor construct.
                                                                                                                                                                                                                                                                                                                                          /*tag= r
/bound moiety= 'nucleotides 2-1'
/mote= "binds nucleotides 2-1 of itself"
                                                                            /*tag= n
|01. .102
|4.tag=
|bound molety= "nucleotides 8-7"
|note="binds nucleotides 8-7 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107 BP; 27 A; 20 C; 26 G; 19 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                             / tag= q // tag= q // bound_molety= "nucleotide 3" // note= "binds nucleotide 3 of itself" 107. 108
                                                                                                                                                                                         /*tag= p
/bound_moiety= "nucleotide 5"
/note= "binds nucleotide 5 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACTCACTATAGGAAGAGATG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 7; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK10821 standard; DNA; 123 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2001, 2001WO-US020557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-2000, 2000US-00605558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNII ) UNIV ILLINOIS FOUND.
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                                                                                                 misc_binding
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                                                                                                                                                                                                                                             misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu Y, Li J;
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                                                              stem_loop
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1D ABK

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AAL45458 standard; DNA; 19 BP.

06-JUN-2002 (first entry)

AAL45458;

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New conjoined polynucleotides comprising a kinase domain and an adenylase domain, useful in DNA cloning, for carrying out sequential polynucleotide manipulations in a serial fashion, or for polynucleotide manipulations.
                                                                                                                                                                                                                                                                                                                                                  //tag= a
/bound_moiety= 'ABK10807'
/boure= 'Porms a double stranded region with the template
strand shown in ABK10807'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a conjoined polynucleotide comprising at least two catalytic domains which function in concert to provide a chemical transformation involving multiple sequential reactions. The use of the conjoined polynucleotides as catalysts offer advanceses over protein-based enzymes in cloning and in a number of commercial and industrial processes. Conjoined polynucleotides made from INA are expected to be such more stable, and can be easily made by automated oligonucleotide synthesis, and DNA is significantly more resistant to hydrolyric their ability to function on solid support and are expected to retain their ability to function on solid support and are expected to retain their activity when immobilised. This sequence represents an acceptor construct used in the selection of self-phosphorylating deoxyribozymes,
                                                                                                                   Self-phosphorylating deoxyribozyme; conjoinad polynuclaotida; catalyst; ribozyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/bound moiety= "Primer 1"
/note= "The sequence for primer 1 is not given in the specification"
                                                             Self-phosphorylating deoxyribozyme selection, acceptor construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *raga c
'notes "Random sequence of 70 nucleotides"
.09. .123

    .24
    /*tag= b
    /note= "Phosphorylation and ligation site"

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                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4B; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0159B08P.
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21-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                 misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer_bind
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                                                                                                                                                                                                                           Synthetic.
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The present invention relates to biosensors, comprising a nucleic acid enzyme dependent on an ion to produce a product, a quencher or/and a fluorophore and a photocodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal ions such as lead. The biosensors may also be used to detectine the concentration of a particular ion in a solution. The present sequence is a substrate of a ribozyme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mew nucleic acid enzyme biosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                       /*tag= b
12. .19
/*tag= c
/bound molety= *RNA-cleaving deoxyribozyme"
/note= "binds nucleotides 8-1 of the deoxyribozyme shown in ANI45457*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
                                                                                                                                                                                                                                              /*tag= a /bound_moiety= "RNA-cleaving deoxyribozyme" /note= blinds nucleotides 41-34 of the deoxyribozyme shown in AAL45457"
                                                                                                                         Biosensor; ion detection; lead; zinc; cobalt; nucleic acid entyme; quancher; fluorophore; photodetector; ion concentration; ribozyme; substrate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                    RNA-cleaving deoxyribozyme substrate #5.
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1, Fig 6, 57pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CTCACTATAGGAAGAGATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CICACIATAGGAAGAGAIG 19
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                                                                                                                                                                                                                  Key
misc_binding
                                                                                                                                                                                                                                                                                                                                 misc_binding
                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lu Y, Li J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002.
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                                                                                                                                                                                                                                                                                                          misc_RNA
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AAV36569
ID AAV36
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14 ACTCACTATAGGAAGAGATG 33

1 ACTCACTATAGGAAGATG 20

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Ouery Match 100.0%; Score 20; DB 6; Length 123; Best Local Similarity, 100.0%; Pred. No. 3.7; Matches 20; Conservative 0; Mismatches 0; Indels

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The present invention relates to biosensors, comprising a nucleic acid ensyme dependent on an ion to produce a product, a quencher or/and a Eluorophors and a photodetector. The biosensors are useful for the sensitive and selective detection of ions. The biosensors are useful in methods of detecting the presence of an ion, particularly metal lons such as laad. The biosensors may also be used to determine the concentration of a particular ion in a solution. The present sequence is a riboryme which may be used as a biosensor of the invention
                                                                                                                                                                                                                                                                                                                        New nucleic acid enzyme blosensors, useful for the sensitive and selective detection of ions, particularly metal ions e.g. lead ions, and for determining the concentration of a particular ion in a solution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensyme, catalysis, cleavage, target, pharmaceutical, medical; substrate; regulator, detergent, dental hygiene, meat tenderiser, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.0%; Score 18.4; DB 6; Length 43; Best Local Similarity 95.0%; Pred. No. 21; Matches 19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43 BP; 15 A; 9 C; 11 G; 8 T; 0 U; 0 Other;
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/note= *ribonuclectide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 ACCCACTATAGGAAGATG 38
                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Pig 3; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzymatic DNA 19mer substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV82933 standard, DNA, 19 BP.
                                                                                                                      27-JUN-2001, 2001WO-US020557
                                                                                                                                                           27-JUN-2000; 2000U8-00605558
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                                                                                                                                                                                                    (UNII ) UNIV ILLINOIS FOUND.
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                                                                                                                                                                                                                                                                                 WPI; 2002-130823/17.
                                      WO200200006-A2
Unidentified.
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misc_RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a self-cleaving DNA molecule HD2 (ribozyme) of the invention. The specification describes an allosteric DNA polymocleotide which can modify a function or configuration of the polymucleotide with a chemical effector and/or a physical signal. This polymucleotide can comprise the present sequence. The allosteric polymucleotides can be used for detecting the presence or concentrations of compounds such as amino acids, peptides, nucleotides, nucleotides, preroids, microbial or cellular metabolites, blood or urine components, pharmaccuticals, pesticides, herbicides, or food toxins. The allosteric polymucleotides can also be used for detecting physical signals such as radiation and temperature changes. The polymucleotides can also be used in biosensors, in which they are more stable than proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allosteric polynucleotides - having modified function or configuration, used for the production of biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosensor; ion detection; lead; zinc; cobalt; nucleic acid enzyme; quencher; fluorophore; photodetector; ion concentration; ribozyme; ss.
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                                                                                                                      Self-cleaving DNA; allosteric DNA polynucleotide; modify; function; configuration; detection; biosensor; ss.
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                                                                                  Self-cleaving DNA (deoxyribozyme) sequence HD2.
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                                                                                                                                                                                                                                                                                 /note= "RNA A linkage"
                                                                                                                                                                                                                          Location/Qualifiers
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97US-0055039P
                                         (first entry)
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08-AUG-1997;
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                                                                                                                                                                                    Synthetic
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specifically cleaves a substrate a uncleic acid at a defined cleavage site, where the catalytic DNA molecule comprises at least one pyramidine uncleotide [1]. [1] is a catalytic DNA molecule, capable of hydrolytic cleavage of a nucleic acid phosphoester bond. The catalytic DNA molecule cleavage of a nucleic acid phosphoester bond. The catalytic DNA molecule is used to cleave RNA of almost any sequence. This is useful for cleavage of single-etranded mucleic acid in the absence of a restriction cleavage of single-etranded mucleic acid in the absence of a restriction argume is composed of only 12 residues, making this one of the ministed argume is composed of only 12 residues, making this one of the smallest nucleic acid catalyses known. The catalytic core of the ministed argume is composed of only 12 residues, making this one of the smallest nucleic acid catalyses known. The catalytic core forms a compact hairpin structure displaying the 3 indiacel-containing residues. The enzyme can be made to cleave RNA of almost any sequence by simple alteration of the two substrate-recognition domains that surround the catalytic core. The caryme operates with multiple turnover the presence of micromolar concentrations of 22.4, exhibiting saturation kinetics and actalytic core uncatalysed reaction. The imidazole-containing DNA enzyme combines the substrate-recognition properties of nucleic acid enzymes and the chemical functionality of proceeds anymes in a molecule that is small in size, yet core transmitting as male acquence represents an expension of the contained sequence which is used in the exemplification of the contained sequence which is used in the exemplification of the contained sequence represents and catalytically efficient. The present sequence of the contained and catalytically efficient. The present sequence of the contained and ca
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/note= "adenosine ribonucleotide"
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                        Example 2; Col 29; 52pp; English.
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mes 18; Conservative
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                                                                                                                                                                                                                                This sequence is used in a method which involves the production of catalytic DNR molecules can be used for cleaving target nucleic acid molecules Such DNR molecules can be used in pharmaceutical and medical products (e.g. for wound debridement, clot dissolution), as well as in household items (e.g. detergents, dental hygiene products, meat renderisers'). Other suitable substrates include those comprising or produced by picornaviruses, hepadraviridae, (e.g. HBV, HCV), papitiomaviruses (e.g. HBV), gammaharpesvirinae! (e.g. HBV, HCV) illymphocryptoviruses (e.g. HPV), gammaharpesvirinae! (e.g. HBV), flaviviruses, togaviruses, increase (e.g. HTV-1 and -11), flaviviruses, cycomegaclviruses (GNV), influenza viruses and betaherpesviruses contributing to immunodeficiency viruses and el. Hiv-1 and -2), simian and felina immunodeficiency viruses and bovine leukemia viruses. They can also be used as regulators of gene
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                                                                     satalytic DNA molecules - having site-specific endomuclease activity substrate nucleic acid, used for cleaving target nucleic acid
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/note= "adenosine ribonucleotide"
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                                                                                                                                                                                      Disclosure; Page 66; 161pp; English
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                                                                           New catalytic
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New complex formed by a hybridization reaction, useful for detecting a nucleic acid sequence of interest in sample, comprises the target nucleic
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17-AUG-1999; 99US-0149176P.
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 WPI; 2000-593449/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a catalytic INA molecule that specifically cleaves a substrate nucleic acid at a defined cleavage site, where the catalytic DNA molecule comprises a part least one pyrimidine catalytic DNA molecule, capable of hydrolytic cleavage of a nucleic acid phosphoester bond. The catalytic DNA molecule is used to cleave RNA of almost any sequence. This is useful for cleavage of a nucleic acid phosphoester bond. The catalytic DNA molecule is used to cleave RNA of almost any sequence. This is useful in methods of andomiclase site at a specific position. This is useful in methods of andomiclase site at a specific position. This is useful in methods of e.g. cloning and genetic engineering. The catalytic core of the smallest nucleic acid catalytes known. The catalytic core of the smallest nucleic acid catalytic state accompact halippin the made to cleave RNA of almost any sequence by simple alteration of the two substrate-recognition domains that surround the actalytic core. The engage of catalytic core in the presence of micromolar concentrations of Zn2+, exhibiting saturation kinetics and a catalytic rate enhancement of approximately inconou-fold compared to the substrate-recognition properties of nucleic acid enzymes and the chemical functionality of protein enzymes in the sequence represents an enjample and catalytically efficient. The present sequence represents an olicinal content and catalytically efficient. The present exemplification of the content and catalytically efficient. The present exemplification of the content of the sequence which is used in the exemplification of the content and catalytically efficient in the exemplification of the content and catalytically efficient in the exemplification of the content of the content and catalytically efficient in the exemplification of the content of the content and catalytically efficient is a small in size, we content the content and catalytically efficient in the exemplification of the content of the content and catalytically efficient
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Ensymatic DNA molecules containing modified nucleotides useful for cleavage of RNA at a specified position.
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/note* "adenosine ribonucleotide"
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                                                    Example 1; Col 7; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA92233;
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Cardy DLN;

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The present invention describes a catalytic DNA molecule that

specifically clasves a substrate nucleic acid at a defined cleavage site,
where the catalytic DNA molecule comprises at least one pyrimidine
nucleotide (I). (I) is a catalytic DNA molecule, capable of hydrolytic
cleavage of a mucleic acid phosphoseter bond. The catalytic DNA molecule
of single-erranded nucleic acid in the absence of a restriction
of single-erranded nucleic acid in the absence of a restriction
of communicate site at a specific position. This is useful in methods of
e.g. cloning and generic engineering. The catalytic core of the minimised
aryme is composed of only 12 residues, making this one of the smallest
nucleic acid catalysts known. The catalytic core of the minimised
enzyme is composed of only 12 residues, making this one of the smallest
nucleic acid catalysts known. The catalytic core forms a compact hairpin
structure displaying the 1 indazole-containing residues. The enzyme can
be made to cleave RNA of almost any sequence by simple alteration. Of the
two substrate-recognition domains that surround the catalytic core. The
concentrations of Zn2+, exhibiting seturation kinetics and a catalytic
crate enhancement of approximately 10000000-fold compared to the
substrate-recognition properties of nucleic acid enzymes and the chemical
concentration and catalytically efficient. The present sequence represents an
concential invention
disponucleotide sequence which is used in the exemplification of the
present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
Ensymatic DNA molecules containing modified nucleotides useful for cleavage of RNA at a specified position.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0%; Score 18; DB 3; Length 19; 100.0%; Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           larity 100.0%; Fred. No. 32, Conservative 0, Mismatches
                                                                                                                                   Example 3, Col 31, 52pp, English.
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AAF60641 standard; DNA; 103 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCACTATAGGAAGATG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 18, Conserv
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The present invention relates to probes complementary to a single strand of an RNA polymerase promoter sequence, and a blocking group adjacent or substantially adjacent to the promoter sequence. The probes are useful for detecting nucleic acid sequence of interest in a sample, for e.g. a nucleic acid which is a marker of genetic or infectious disease. The present sequence is one such probe which was used in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel probe molecule useful for detecting nucleic acid sequence in a sample, comprises single stranded nucleic acid sequence complementary to target sequence, RNA polymerase promoter sequence, and blocking group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA polymerase promoter; probe; disease marker detection; ss.
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90.0%; Score 18; DB 5; Length 111;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardy DLN, Marsh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2, Page 17; 59pp; English.
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AAF60604 standard; DNA; 111 BP.
                                                                                   1590/c
AAF60590 standard; DNA; 111 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACTCACTATAGGAAGAGA 18
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                                                                                                                                                                                                                                                                                         entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lloyd JS, Weston A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CYTO-) CYTOCRLL LTD
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                                                                                                                                                                                                                                                                                    (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
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                                HESULT 37

AAP60590/
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AMPROSO4/
AMPR
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                                                                                                                                              The present invention relates to a complex formed by the hybridisation of a target nucleic acid (e.g. a bacteriophage RNA polymerase promoter sequence) and probes. The probes are useful in an assay for detecting the presence of a nucleic acid sequence of interest, in a sample. The present sequence is a probe which was used in the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ů
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 103 BP; 22 A; 26 C; 19 G; 36 T; 0 U; 0 Other;
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                                                                              Example 6; Page 27; 58pp; English.
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acid molecule and 2 or 3 probes.
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Best Local Similarity 100.
Matches 18; Conservative
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Probe #3.

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Novel probe molecule useful for detecting nuclaic acid sequence in a sample, comprises single stranded nucleic acid sequence complementary to target sequence, RNA polymerase promoter sequence, and blocking group.
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present sequence is one such probe which was used in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA polymerase promoter; probe, disease marker detection, ss.
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Pred. No. 35,
0, Mismatches 0, Indels
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                                                            Sequence 111 BP, 13 A, 35 C, 21 G; 42 T; 0 U; 0 Other;
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Job time : 124.019 secs
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100.0%; Pre
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                                                                                                                                                                                Novel probe molecule useful for detecting nucleic acid sequence in a sample, comprises single stranded nucleic acid sequence complementary to target sequence, RNA polymerase promoter sequence, and blocking group.
                                                                                                                                                                                                                                                                                                     The present invention relates to probes complementary to a single strand of an RNA polymerase promoter sequence, and a blocking group adjacent or substantially adjacent to the promoter sequence. The probes are useful for detecting nucleic acid sequence of interest in a sample, for e.g. a nucleic acid which is a marker of genetic or infectious disease. The present sequence is one such probe which was used in the present
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                                                                                                      Marsh Pr
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                                                                (CYIO-) CYTOCELL LID.
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                             29-JUL-1999;
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                                                                                                           Lloyd JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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AAF60596/
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EST38345 EST38335 EST385360 EST382001 HNC8-1-G1 EST391208 EST39123 EST384869

EST381974 HNC8-1-G1 EST382183

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Run or:

Sequence:

Searched:

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Macaca mulatta (Thesus monkey)
Macaca mulatta (Thesus monkey)
Macaca mulatta (Thesus monkey)
Macaca mulatta
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Cararthini; Cercopithecidae;
Carcopithecinae; Macaca.

I (bases 1 to 612)
SINCI-CAGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAD),
Thunor Gane Index

NAT Unpublished (11997)
Contact: Daniela & Gerhard, Ph.D.
Office of Cancer Genomics (NIH
Bldg. 31 RANIOAD7 Betheseda, MD 20892
Email: CgaDbs-r@mail.nih.gov
Tissue Procurement: Inv. Tony M. Plant
CDNA ibbrary Preparation: Invitorgen Corp
CDNA ibbrary Preparation: Invitorgen Corp
CDNA ibbrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
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Macaca mulatta cDNA clone
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AGENCOURT 14714597 NICHD Rh Test2 |
CD767851 GI:32426353
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RESULT 1
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  C3767851 AGENCOURT
CD071925 MA2-0036G
AQ430253 HS 5078 B
AA567751 HL01719.5
                                                                                                                     May 24, 2004, 10:22:21; Search time 1104:53 Seconds (without alignments) 540.723 Million cell updates/sec
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                GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                 Bukaryota, Matazoa; Platyhelminthes; Trematoda; Digenea; Bukaryota, Matazoa; Platyhelminthes; Trematoda; Ghistosoma.

1 (Dases 1 to 459)

Verjovski-Almeida, B., DeWarco, R., Martins, B. A.L., Gulmaraes, P. E.N., Olopi, B. P. B., Paquola, A. C.M., Piazza, J. P., Nishiyama, M. Y. Jr., Kitajima, J. P., Adamson, R. B., Sahton, P. D., Bonaldo, N. P., T. Kitajima, J. P., Dillon, B. P., Farias, L. P., Regorilo, S. P., E., Matagasto, P. A., Malaquias, L. C., Narques, R. C., Mishiyasa, M. Y. Jr., Nachmento, A. L. T. O., Ollveiler, P. P., Fasis, B. M., Ribeiro, M. A., Sa, R. G., Stukart, G. C., Soares, N. B., Gargioni, C., Kawaro, T., Setubal, J. C., Leite, L. C. C. and Dias-Neto, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD071925

MA2-0036G-V373-G02-U.B MA2-0036 Schistosoma mansoni cDNA clone
MA2-0036G-V373-G02.B, mRNA sequence.
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Pax: +55-11-3091-2186

Email: verjodiquup.br

This sequence was derived from the FAPESP Schistosoma mansoni EST

Genome Project. All sequences in the project ware assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
Brasil
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Contact: Mahairas GG, Wallace JC, Hood L.

Contact: Mahairas GG, Wallace JC, Hood L.

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
781: (206) 616-3887

Emai: jvallace@u.vashington.edu
Clones are derived forme the human BAC library RPCI-11. For BAC
11brary availability, please contact Pieter de Jong
(pieter@dejong.med.bufsalo.edu). Clones may be purefased from
RCPAC Resources (http://war.htsc.ore.bufsalo.edu). clones was be purefased from
BACPAC Resources (http://war.htsc.ore.bufsalo.edu). BAC end Web_Server:
Plate: 654 row: D column: 17
Seq primer: T7
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1 (bases 1 to 556)
Mahairas, G.G., Mallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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/note="Vector: pBACe3.6, Site 1: EcoR1; Site 2: EcoR1;
Male blood DRA was isolated from one randomly chosen donor
and partially digested with a combination of EcoR1 and
EcoR1 Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoR1 sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-Lagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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HS_5078_B1_B09_T7 RPCI-11 Ruman Male BAC Library Hono sapiens
genomic clone Plate=654 Col=17 Row=D, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                   Gape
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                                                                                                                                                                                                                                                                                                                  Query Match 87.3%; Score 17.4; DB 14; Best Local Similarity 94.7%; Pred: No. 5.3e+D2; Matches 18; Conservative 0; Mismatches 1;
                /mol type="mRNN"
/db Xref="taxon:6183"
/clone="MAZ-0036G-V373-G02.8"
/sex="mixed pool"
/dev stage="adult"
/lab_lost="Wax=0036"
/note="Vector: pGBM T-easy"
'organism="Schistosoma mansoni"
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|mol_type="genomic DNA"
|db_xref="taxon:966s"
|clone="plate=654 Col=17 Row=D"
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Class: BAC ends
High quality sequence stop: 556.
Location/Qualifiers
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Homo sapiens
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lorganisme."Arabidopsis thaliana"

| organisme."Arabidopsis thaliana"
| origivar="C24"
| or
                         Eukaryota Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Byermatophyta; Wagmollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 [bases 1 to 55] Brassicales; Brassicaceae; Arabidopsis.

2 [bases 1 to 55] Brassicales; Tracke, R.; Torjek, O.; Altmann, T.; Micchell-Olds, T. and Weisshaar, B.

Micchell-Olds, T. and Weisshaar, B.

Sarge-scale identification and analysis of genome wide single-nucleotide polymorphisms for mapping in Arabidopsis thalians Genome Res. 13 (6), 120-1257 (2003)
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Ex2304.yl Zebrafish C32 14 somite embryo Danio rerio cDNA clone
IMAGE:5620495 5', mRNA sequence.
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( Charloformes; Cyprinidae; Danio.

1 ( Lasee 1 to 90)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marrs,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Weisshaar B
ADIS DNA core facility at MPIZ
AMX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Pax: 004922150620851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 55 Std Brror: 0.00
Plate: 14 row: F column: 21
Seq primer: pBl21, GGTGGGGGCGCTTAG.
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90.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 2;
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Danio rerio
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Best Local Similarity 90.07
Matches 18; Conservative
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BM778744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS67751 496 bp mRNA linear EST 19-APR-2001 1601119. Sprime HL Drosophila melanogaeter head BlueScript Drosophila melanogaeter cDNA clone HL01719 5prime, mRNA sequence. AAS67751
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//ocome land-brain & searsory organ; Vector:
blueScript SK, Site 1: EcoRI; Site 2: Khol; Constructed
using Strategene ZAP-cDNA Synthesis kit. Oligo dT-primed
and directionally cloned at EcoRI and XhoI in BlueScript
SK(+/-)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Brosophila melanogaster
Brukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Endopterygota; Brosophila;
Bphydroidea; Drosophilae; Drosophila.
1 (bases i to 496)
14 (bases i to 496)
15 (bases i to 406)
16 (bases i to 406)
16 (bases i to 406)
17 (bases i to 406)
18 (bases i to 406)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Eax: 510 466 6798
Email: http://www.fruitfly.org/BST, estefruitfly.berkeley.edu
Plate: 17 row: B column: 7
High quality sequence stop: 322.
Location/qualifiers
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Contact: Stapleton, M.
BDGP
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                              Query Match
Best Local Similarity 94.7%; Pred. No. 5.78+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0;
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Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels
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Coganism=Drosophila melanogaster=
| mol_type="mRNA" |
| db_xref="BDSP_EST:BDcln022638" |
| db_xref="taxon:7227" |
| cone="HL0119" |
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/dev stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                        2 CTCACTATAGGAAGAGATG 20
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CB261880/c
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BE837087

146 bp mRNA linear EST 22-SBP-2000

ECC.-FN0089-060600-011-d03 FN0089 Homo sapiens CDNA, mRNA sequence
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1. (Dases 1 to 146)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Madai, M.A., da Sliva, M. Jago, M.A., Bardih, S., Costa, F., Goldman, G. H., Carvalho, A.F., Mateukuma, A., Baia, G.S., Sinpson, D.H., Purnatein, A., deOliveira, P. S., Bucher, P., Jongeneel, C.V., Surae, M.J., Soares, P., Brentani, R., Rais, L.F., de Souza, S. J. and Sinpson, A.J.
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Tel: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

[http://www.ludwig.org.br/sezipts/gethtml2.pl?tl=&tc2=RC2-FN3389-065
600-011-d03st3=25000-06.ef4=1;
9eg primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                          GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay kumar-1@gsk.com
Seq primer: 77.
                                   Sathe, G., Mui, P., Agarwal, P., Badger, R.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORP expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 {7}, 3491-3496 (2000)
20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Ranlo-SP,
                                                                                                              Identification and initial characterization of 5000 expressed expensed tags (ESTs) each from adult human normal and osteoarthritic cartilage CDNA libraries
Osteoarthritic Cartilage (T), 641-653 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo mapiens"
/mol_type="maxM="
/mol_type="maxM="
/doloretype="cartilage"
/lab_hogt="E.coli DH10 g="
/colorellb="HOM (Human Osteoarthritic Cartilage)"
/note="Wettor: pSPORT 1; Site_1: Sall; Site_2: Not1:
Directional"
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BB837087.1 GI:10269465
                                                                                                                                                                                                                                                                                                                                               Contact: Sanjay Kumar
UM2109
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Homo sapiens
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Eddy, S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Underwood, K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Earvey, N., Schurk, R., Marcerstor, R. and Wilson, R., Jackson, Y., Cardenas, M., McCann, R., Watterstor, R. and Wilson, R., Wathu Zabratich Est Project 1998

Unpublished (1998)

Unpublished (1998)

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Unversity School of Medicine
Wathuron University School of Medicine
Wathuron University School of Medicine
Wathuron University School of Medicine
Tal: 314 286 1800

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//db xref="taxon:7955"
//ide="INAGE-5620495"
//issue_repe="embryo, 14 somite"
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Bukaryots, Meransa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101)
Kumar, S., Cohnor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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84.01; Score 16.8; DB 12; Length 90;
Best Local Similarity 90.01; Pred. No. 5.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
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/mol_type="mRNA"
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BG899265.1 GI:14309514
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RC2-FN0089-160600-014-h07 FN0089 Ношо sapiens CDNA, mRNA sequence.
BB837170
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Jane Neto, B., Garcia, Correa, R., Verjoveki-Aimeida, S., Briones, R.R., Nagai, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P. Matunkuna, A., Baia, C. S., Simpson, D.H., Burnstein, A., deoliveira, P. B., Jongenesl, C. V., Soura, D.H., Whenkein, A., deoliveira, P. B., Bucher, P., Jongenesl, C. V., Goliveira, P. Brentani, R.R., Reis, L.F., de Soura, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Tel: +55-11-2704922
Bmall: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
This entry can be seen in the following URL
(http://www.ludwig.org.br/serripts/gethtml2.pl?tl=&t2=RC2-FN0089-160
600-014-h07&tl=2000-06-16&t4=1)
Righ quality sequence start: 31
High quality sequence start: 31
High quality sequence etop: 252.
1. 252
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Smal; Site_2: Smal; Afmin-library was made by closhing
products derived from ONESTES PCR (U.S. Letters Patent
application No. 196;716 - Ludwig Institute for Cancer
Research, profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rus Frof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORP expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2002)
20202663
Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
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Best Local Similarity 90.0%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                         Length 247;
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                                                                                                                      ch 84.04; Score 16.8; DB 10; I Similarity 90.04; Pred. No. 8.2e+02; 18; Conservative 0; Mismatches 2;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                         162 ACTAACCATAGGAAGAGATG 181
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Homo sapiens
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/ Corganisms-Homo sapiens"

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/ db_xrefs=texcn:9606"

/ dev_sisges=Adult=""

/ clone_libs=Pr0089"

/ notes=Torgan: prostate_normal, Vector: pucl8; Site_l:

/ clone_libs=Pr0089"

/ notes=Torgan: A mini_library was made by cloning

smal; Site_l: Smal; A mini_library was made by cloning

products derived from ORHSTES FCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions.
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High quality sequence stop: 146.
Location/Qualifiers
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Plate: 63 row: P column: 19
9eq primer: ATTTAGGTGACACTATAG.
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BG927617 409 bp mRNA linear EST 06-NOV-2001
HNC41-1-G12.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
                                      Contact: Sanjay Kumar
Contact: Sanjay Kumar
UNAZO9
GJANZO9
GJANZO9
TO9 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
PAX: 610-270-7558
Rmail: sanjay-kumar-10gsk.com
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kumar,S., Comnor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,J., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA Tel: 610-270-7245
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Marmalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 409)
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Directional"
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/core lib="HOM (Human Ostecarthritic Cartilage)"
/note="Yector: pSFORT I; Site_1: Sall; Site_2: Notl;
Directional"
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Osteoarthr. Cartil. 9 (7), 641-653 (2001)
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Bmail: Banjay kumar-1@gsk.com
Seg primer: T7.
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MRN17-1-812 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,
BG897743
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                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryote; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi; Nammalia; Butheria; Primaces; Catarrhini; Hominidae; Homo. 1 (bases 1 to 355) Hogde, P., Gl.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.S., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
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                                                                       Gaps
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                                                                  Indels · 0;
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84.0%; Score 16.8; DB 10; Length 355;
Best Local Similarity 90.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0
                               Length 335;
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The Institute for Genomic Research
9712 Wedical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Pax: 301 638 0208
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                            Query Match

Best Local Similarity 90.0%; Pred. No. 9.2e+02;
Matches 18; Conservative 0; Mismatches 2;
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Manalist Substances, Chordata, Craniata, Vertebrata; Buteleostomi, Manmalist Subtaryota; Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi, Manmalist Subteria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (Dases I to 4:12).

E. 1 (Dases I to 4:12).

Hodda, P., Ol.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Ouackenbush, J.

Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

L. Unpublished (2000)

Contact: John Quackenbush

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File 1301 838 1528

Fax: 301 838 0208

Email: John Quickenbush

Pare: 271
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HNCB-1-G10.R HNC (Human Mormal Cartilage) Homo sapiens CDNA, mRNA
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84.0%; Score 16.8; DB 10; Length 421;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
781: 301 838 3528
824: 301 838 0208
Email: Johng@tigr.org
                                                                                                                          Seq primer: Forward.

Location/Qualifiers

Location/Qualifiers

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forganisma-Homo sapiens"
/organismanka.
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EST385360 MAGE resequences, MAGM Homo sapiens cDNA, mENA sequence.
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AN973262.1 GI:8163120
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 42)
Hegde, P., Qi,R., Abernathy,K., Oharap,S., Gaspard,R., Gay,C., Holt, I.B., Saced,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
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                 Query Match 84.0%; Score 16.8; DB 12; Length 409; Best Local Similarity 90.0%; Pred. No. 1e+03; Matches 18; Conservative 0; Mismatches 2; Indels 0
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84.0%; Score 16.8; DB 10; Length 416;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0
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1. 416
1. 416
7. Granisma-Homo sapiens"
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Contact: John Quackenbush
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Homo sapiens
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AM979113 AAGE reseguences, MAGP Homo sapiens CDNA, mRNA seguence.
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BST184189 MAGE resequences, MAGE Homo saplens cDNA, mRNA sequence.
AW971980
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Bukaryotta, Metratoa, Chordata, Craniata, Vertebzata, Euteleostomi,
Bukaryotta, Metratoa, Chordata, Craniata, Vertebzata, Euteleostomi,
Mammalia, Butberia, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 439)

1 (bases 1, C4, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I. B., Sased, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
Quackenbush, J.
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria; Primates, Catarrhini, Hominidse, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Pax: 301 838 0208
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                                                                                                                                                                                            Length 438;
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                                                                                                                                                                                       Ouery Match 84.0%; Score 16.8; DB 10; Length Best Local Similarity 90.0%; Pred. No. 1e+03; Matches 18; Conservative 0; Mismatches 2; Indels
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mol_type="makk" |
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Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                            401 ACTCACTATAGGAAAAGCTG 382
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Plate: 402
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ACCESSION
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AW979113/c
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AW971980/c
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AUTHORS
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                                                                                                                Eukaryofa, Netazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 434)
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, M., Van Horn, M., Nao, J., Satha, G., Mui, F., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.
                                                                                                                                                                                                                                                                                                                                                                                             GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Pax: 610-270-5598
Email: sanjay kumar-lægsk.com
Seq primer: T7.
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Bomo sapiens
Bukaryota; Metazoa Chordata; Craniata; Vertebrata; Euraleostomi;
Bukaryota; Metazoa Chordata; Craurinin; Hominidae; Homo.

(bases 1 to 418)
Hegde, P., Ol.R., Abernathy, K., Dharap, S., Gaspard, B., Gay, C.,
Holt, I.E., Saeed, A.I., Sharov, V., Les, N.H., Yestman, T.J. and
Ouackenbush, J.
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Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                              Identification and initial characterization of 5000 expressed sequenced tags (BSTs) each from adult human normal and osteoarthritic cartlage cDNA libraries osteoarthr. Cartil. 9 (7), 641-653 (2001)
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/mol_type="mRNA"
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/note="Vector: pSPORT I; Site_1: Sali; Site_2: Not1;
Directional"
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Pred. No. 1e+03;
0; Mismatches 2; Indels 0
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                                   3G927056.1 GI:14321579
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                                                                                                                                                                                                                                                                                                                                                                          Contact: Sanjay Kumar
JW2109
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Plate: 402
Seq primer: Porward.
                                                                       Homo sapiens (human)
         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANIEM
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AW979098/c
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AUTHORS
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PUBMED
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셤 8

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

PRATURES

ORIGIN

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Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butbaria; Primates; Catarthin; Hominidae; Homo.

B. 1 (bases 1 to 446)

B. 16ases 1 to 446)

Guackenbush, J. Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Rolt, I. K., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.

Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

Unpublished (2000)

Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, YD 20850, USA

Pax: 301 838 3528
                                                                                                                                                                                                          AM972775 446 bp mRNA linear EST 01-JUN-2000 ST184869 MAGE resequences, MAGE Homo sapiens CDNA, mRNA sequence. AM972775
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Homo sapiens
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 459)

Hegde, P., Ol.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,

Hole, I.E., Sased, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and

Quackenbush, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .446 | Organism="Homo sapiens" | Organism="Romo sapiens" | Omol_type="RONA" | Omol_type="RONA" | Omole="Faxon:9606" | Clone lib="MAGB resequences, MAGL" | Oncte="Vector: pBluescriptsKm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Porward.
Location/Qualifiers
   428 ACTCACTATAGGAAAGTTG 409
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Plate: 310
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Homo sapiens
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AM972775/C
LOCCE
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AW974684/c
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1 (bases 1 to 441)
Hegde, P., Oli,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Ouackenbush,J.
Assessment of gens expression patterns in a model of colon tumor
metastasis using a 19,200 element cunw microarray
Unpublished (2000)
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                                                                                                                                                                                                                          Contact: John Quackenbush
The Institute for Genomic Research
The Institute for Genomic Research
Tol: Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3228
Fax: 301 838 0208
Email: johnq@tigr.org
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/organism="Nomo sapiens"
/molltype="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGK"
/note="Vector: paluescriptsKm"
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Location/Qualifiers
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Plate: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
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Hest Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holt, I.E., Sa
Quackenbush, J
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LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

PEATURES

ORIGIN

RESULT 26 AW969893/c

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PEATURES

ORIGIN

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AM970102 473 bp mRNA linear EST 01-JUN-2000
EST82183 MAGE resequences, MAGK Homo sapiens CDNA, mRNA sequence.
AM970103
  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Duteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Bomo.

1 (bases 1 to 463)

Kumar, B., Connor, J.R., Dodds, R.A., Halsey, M., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M. W.

Identification and initial characterization of 5000 expressed esquenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
                                                                                                                                                                                                                                                                                              UNZ109
GlawoZhithKilne
GlawoZhithKilne
709 Swedeland Road, P.O. Box 1519, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Pax: 610-270-5598
Email: sanjay kumar-10gsk.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
Bukaryota Metazoa Chordata, Craniata, Vertebrata, Euteleostomi;
Bukaryota Metazoa Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Euheria, Primates; Catarrhini, Hominidae, Homo.

1 (bases 1 to 473)
Hegde, P., Ol, R., Abernathy, K., Jharap, E., Gaspard, R., Gay, C., Holt, I.E., Sased, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Conteat: John Quecklenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Pax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

84.0%; Score 16.8; DB 12; Length 469;
Best Local Similarity 90.0%; Pred. No. 1.18+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers

1. 473
/ Coganiam="Homo sapiens"
/ Mol type="mRNA"
/ AD_Xref="taxon:9606"
/ clone_lib="WAGB resequences, WAGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                              Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bmail: johnq@tigr.org
Plate: 273
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AM970102/c
LOCUS
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AUTHORS
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PUBMED
COMMENT
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AUTHORS
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                                                                                                                                      TITLE
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SET3181974 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.
AM969896
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HNC8-1-G12.R ENC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (bases 1 to 463)
Hodden, Catarrhini, Hominidae, Homo.

2 (bases 1 to 463)
Hold, H., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I.E., Saced, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assessment of gene expression patterns in a model of colon tumor metastessis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
Chairitute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Exail: johnq@tigr.org
                                                                                                                                                                                                                                                                            Gapa
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84.0%; Score 16.8; DB 10; Length 459;
Best Local Similarity 90.0%; Pred. No. 18+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

84.0%; Score 16.8; DB 10; Length 463;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18, Conservative 0, Mismatches 2; Indels 0,
                                     1. .463
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/mol_trf="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGK"
/note="Vector: pBluescriptSKm"
                      Location/Qualifiers
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BG927057.1 GI:14321580
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Seq primer: Forward
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Homo sapiens
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ACCESSION VERSION KEYMORDS SOLRCE ORGANISM

DEPINITION

RESULT 30

δ 셤 BG927057

DEFINITION VERSION KEYWORDS SOURCE ORGANISM

REPERENCE AUTHORS

COMMENT

TITLE

FEATURES

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AW969896/c LOCUS

RESULT 29

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AW971417

BST381506 WAGE resequences, MAGL Homo sapiens CDNA, mRNA sequence.
AW711417
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1 (bases 1 to 480)
Hegde, F., Ol, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.B., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assessment of gene expression patterns in a model of colon tumor metatersis using a 19,200 element cDNA microarray (Appliance (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 9528 Pax: 301 838 0208 Email: johnqetigr.org
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Query Match 84.0%; Score 16.9; DB 10; Length 480; Best Local Similarity 90.0%; Pred. No. 1.1e+03; Natches 18; Conservative 0; Mismatches 2; Indels 0
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Best Local Similarity 90.0%; Pred. No. 1.18+03;
Matches 18; Conservative 0; Mismatches 2; Indele
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/mol_type="nENA"
/wb.xref="taxon:9506"
/clone lib="MAGE resequences, MAGL"
/note="Vector: pBlueseriptsKz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .480
/organism="Romo sapiens"
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Homo sapiens
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AW971417/c
               JOURNAL
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AUTHORS
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AW969872/c
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Name sapiens

Bukaryota; Metaros; Chordata; Craniata; Vertebrata; Buteleostomi;

Ramalia; Butharia;

1 (bases 1 to 476)

1 (bases 1 to 476)

1 (bases 2); Ol, R., Abernathy, R., Dharap, S., Gaspard, R., Gay, C., Nolt, I.S., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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1 (bases 1 to 478)

Hegde, P., Olik, Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Bolt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.

Assessment of gene expression patterns in a modal of colon tumor metastasis using a 19,200 element cDNA microarray
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Contact: John Quackenbush
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tlgr.org
                                                                                                                                                        Gaps
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1..476
/organism="Homo sapiens"
/mol_type="mRNA" so for the feet state; the feet state; the feet state; how for the feet state; how for the feet state; how for the feet state sta
                                                                                      Query Match 84.04; Score 16.8; DB 10; Best Local Similarity 90.04; Pred. No. 1.1e+03; Matches 18; Conservative 0; Mismatches 2;
            /note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                     444 ACTCACTATAGGAAAAGCTG 425
                                                                                                                                                                                                   1 ACTCACTATAGGAAGAGATG 20
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AW970875.1 GI:8160720
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AW976505/c
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496 bp mRNA linear BST 01-JUN-2000 BST381938 MAGE resequences, MAGE Homo sapiens CDNA, mRNA sequence. ANGS9860.1 GI:8159704 BST.
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EST385858 MAGE resequences, MAGM. Homo sapiens CDNA, mRNA sequence.
AN973757.1 GI:8164942
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Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 [bases 1 to 496]
1 [bases 2, Q1, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.B., Saed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quarkenbush, J.
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Homo sapiens
Homo sapiens
Homo sapiens
Enwarpota, Metarca; Chordata, Craniata, Vertebrata; Enteleostomi;
Enwarpota, Metarca; Chordata, Ctarthini; Hominidae; Homo.
Homenalis, Entheria, Primates, Catarthini; Hominidae; Homo.
Hogde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Osackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
                                                                                                  Query Match
84.0%; Score 16.8; DB 10; Length 495;
Best Local Similarity 90.0%; Pred. No. 1.18+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: John Quackenbueh
The Institute for Genomic Research
Tha Institute for Genomic Research
Tal: Medical Center Dr., Rockville, MD 20850, USA
Tal: 301 838 528
Fax: 301 838 0208
Email: johnq@tigr.org
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84.0%; Score 16.8; DB 10; Length
Best Local Similarity 90.0%; Pred. No. 1.18+03;
Matches 18; Conservative 0; Niematches 2; Indels
              /clone_lib="MAGB resequences, MAGM"
/note="Vactor: pBluescriptSKm"
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Location/Qualifiers

1. .496
/organism="Homo sapiens"
/no_type="manna"
/db_aref="taxon:9606"
/clone_lib="MAGR resequences, MAGK"
/note="Vector: pBluescriptsKm"
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                                                                                                                                                                                   1 ACTCACTATAGGAAGAGATG 20
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Homo sapiens

Homo sapiens

Bukaryota; Wetazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Wetazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Meammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Regdeb.P., Oli, R., Abornathy, K., Dharap, S., Gaspard, R., Gay, C., Holt.I.E., Saeed, A.I., Sharov, V., Lee, M.H., Yeatman, T.J. and Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

Contact: John Quackenbush

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Fax: 301 B38 3228

Fax: 301 Lancaira
AM969872 487 bp mRNA linear RST 01-JUN-2000 R87381950 WAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
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mRNA sequence.
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                                                                                                                                                                                                                                                                         Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
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Fal: 301 838 3528
Fax: 301 838 0208
Fax: 101 938 1259
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Best Local Similarity 90.0%; Pred. No. 1.16+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Momo sapiens"
/organism="Momo sapiens"
/mol_type="mixAx"
/mol_type="mixAx"
/clone_lib="WAGE resequences, WAGK"
/note="Vector: pBluescriptsKm"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Location/Qualifiers
1. .495
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Plate: 315
                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: Forward
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AW973174/c
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AM979054 495 NAGE resequences, MAGP Homo sapiens CDNA, mRNA sequence.
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Homo saplens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia, Eulberia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
Hegde, P., Oi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt., B., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
                                                                                                                                                                                                                                                                                    Assessment of gene expression patterns in a model of colon tumor metaclessis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA rel: 301 838 3528
Fax: 301 838 0208
Email: johnquerigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 84.0%; Score 16.8; DB 10; Length 499; Best Local Similarity 90.0%; Pred. No. 1.18+03; Matches 18; Conservative 0; Mismatches 2; Indels 0
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                                                                          AW979054
AW979054.1 GI:8170338
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Homo sapiens
Bukaryota; Meratoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Meratoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)
1 (bases 1 to 497)
1 (bases 1 to 497)
1 Holt. I. B., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Ouackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assessment of gene expression patterns in a model of colon tumor metastrals using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 9528
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84.04; Score 16.8; DB 10; Length 497;

Best Local Similarity 90.04; Pred. No. 1.18+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0;
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metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Hedical Center Dr., Rockville, MD 20850, USA
Tel: 301 638 9528
Fax: 301 638 0208
Email: johnqëtjgr.org
                                                                                                                                                                       Seq primer: Porward.
Location/Oualiflers

/ Organism="Homo sapiens"
/ nol type="mRNA"
/ db &refe="raxon:9606"
/clone lib="MadE resequences, MAGM"
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Plate: 346
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